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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:22:43 : Search time 39 Seconds
(without alignments)
2244.760 Million cell updates/sec

Title: US-09-863-818a-12

Perfect score: 3512

Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLECSRLERARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_101002.*

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
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- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3512	100.0	657	23	AAU11356 Human DNAX cytokin
2	2711	77.2	667	23	AAU04957 Human Interleukin
3	2711	77.2	667	23	AAU083601 Human PRO protein,
4	1831.5	52.1	617	21	AAU76048 Murine skin cell p
5	1831.5	52.1	617	22	AAU55987 Skin cell protein,
6	1831.5	52.1	617	23	AAU72187 Murine protein iso
7	1108	31.5	226	23	AAU83238 Novel secreted pro
8	948.5	27.0	330	21	AAU75947 Murine skin cell s
9	948.5	27.0	330	22	AAU55886 Skin cell protein,
10	948.5	27.0	330	23	AAU72086 Murine protein iso

11	547	15.6	353	22	ABG08185	Novel human diagno
12	438	12.5	145	22	ABG08183	Novel human diagno
13	435.5	12.4	243	23	AAU11357	Mouse DNAX cytokin
14	318	9.1	698	23	ABU72297	Murine protein iso
15	318	9.1	698	23	AAU11354	Mouse DNAX cytokin
16	313	8.9	698	23	AAE14560	Murine cytokine re
17	312.5	8.9	674	23	AAE14559	Murine cytokine re
18	311	8.9	720	23	AAU98781	Human full length
19	309	8.8	698	23	AAU99161	Mouse interleukin
20	304.5	8.7	692	22	AAU61880	Human cytokine rec
21	304.5	8.7	692	23	AAE14562	Human cytokine rec
22	300	8.5	705	23	AAU98792	Human interleukin
23	299	8.5	705	22	AAU29322	Human PRO polypept
24	299	8.5	705	22	AAU04956	Human Interleukin
25	299	8.5	705	22	AAU61884	Human Interleukin
26	299	8.5	705	22	AAU61884	Human PRO20040. H
27	299	8.5	705	23	ABU5604	Chimeric zcytor14
28	299	8.5	705	23	ABU84998	Human anglogenesis
29	292	8.3	683	23	AAU98789	Human PRO20040 pro
30	288	8.2	703	23	AAU98791	Human Interleukin
31	284	8.1	675	22	AAU61885	Human Interleukin
32	281	8.0	703	23	AAU11353	Chimeric zcytor14
33	278.5	7.9	688	22	AAU61883	Human DNAX cytokin
34	274.5	7.8	187	22	AAU23494	Chimeric zcytor14
35	274	7.8	575	22	AAU61881	Human EST encoded
36	248	7.1	693	23	AAU98790	Human variant zcyt
37	173	4.9	553	23	AAU98788	Human Interleukin
38	155.5	4.4	409	23	AAU98787	Human Interleukin
39	153	4.4	204	22	AAE10920	Human gene 12 enco
40	137.5	3.9	539	23	AAU47457	Human IL-17 recept
41	136	3.9	372	23	AAU98786	Human Interleukin
42	134	3.8	348	23	AAU98785	Human Interleukin
43	133	3.5	866	17	AAU04185	Human Interleukin
44	123	3.5	866	19	AAU61272	Human Interleukin
45	123	3.5	866	20	AAU92409	Human IL-17 prote

ALIGNMENTS

RESULT 1
AAU11356
ID AAU11356 standard; Protein; 657 AA.
AC AAU11356;
XX
XX
DT 26-MAR-2002 (first entry)
XX
XX
DE Human DNAX cytokine receptor subunit 9 (DCRS9) polypeptide.
XX
XX
KW Human; DNAX cytokine receptor subunit 9; DCRS9; phosphate labelling;
KW gene therapy; protein therapy; immunological disorder.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200190358-A2.
XX
XX
PD 29-NOV-2001.
XX
XX
PF 23-MAY-2001; 2001WO-US16767.
XX
XX
PR 24-MAY-2000; 2000US-206862P.
XX
XX
PA (SCHE) SCHERING CORP.
XX
XX
PI Gorman DM;
XX
XX
DR WPI; 2002-106198/14.
DR N-PSDB; AAS18136.
XX
XX
PT Isolated antigenic human or mouse DNAX receptor subunit-like
PT polypeptide useful for detecting antibodies generated in response to
PT presence of increased protein levels or immunological disorders -

XX PS Claim 1; page 29; 148pp; English.

XX CC The invention relates to primate and rodent DNAX cytokine receptor

CC subunit (DCRS) polypeptides and the polynucleotides encoding them. The

CC receptors, or their portions may be useful as phosphate labelling enzymes

CC to label general or specific substrates. The subunits may also be

CC functional immunogens to elicit recognising antibodies, or antigens

CC capable of binding antibodies. A combination, e.g., including a DCRS can

CC be used as an immunogen for the production of antisera or antibodies

CC capable of distinguishing between other cytokine receptor family members.

CC A purified DCRS can also be used as a reagent to detect antibodies

CC generated in response to the presence of elevated levels of expression,

CC or immunological disorders which lead to antibody production to the

CC endogenous receptor. This sequence represents the human DCRS9

CC polypeptide.

XX SQ Sequence 657 AA;

Query Match 100.0%; Score 3512; DB 23; Length 657;

Best Local Similarity 100.0%; Pred. No. 6.8e-313;

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSSRLAALLPLLLIVIDLSDSAGTGFRRHPLHNTRCPPLASHTVLPISLAAPGGPSP 60

Db 1 MGSSRLAALLPLLLIVIDLSDSAGTGFRRHPLHNTRCPPLASHTVLPISLAAPGGPSP 60

QY 61 QSLGVCESTVPACVASICQVAVNGASSTSWCRNPKSLPHSSSIGDTRCQHLLRGSC 120

Db 61 QSLGVCESTVPACVASICQVAVNGASSTSWCRNPKSLPHSSSIGDTRCQHLLRGSC 120

QY 121 CLVVTCLRRRAITPPSPQTSPTDFALKGNLRIQRHGKVFDPDTHKGMVEGTGYNRRWV 180

Db 121 CLVVTCLRRRAITPPSPQTSPTDFALKGNLRIQRHGKVFDPDTHKGMVEGTGYNRRWV 180

QY 181 QLSGGPEFSDLLPEAIRIVTISSGPEVSRLCHOWALECELSPPDYQKIVSGGHV 240

Db 181 QLSGGPEFSDLLPEAIRIVTISSGPEVSRLCHOWALECELSPPDYQKIVSGGHV 240

QY 241 ELPEYFLLPCLCEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYQSHTQVMAL 300

Db 241 ELPEYFLLPCLCEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYQSHTQVMAL 300

QY 301 TLRCPLKLEALCQRHDWHTLCKDLPNATARESNGVYVLEKVDLHPQLCFKVPWFSGN 360

Db 301 TLRCPLKLEALCQRHDWHTLCKDLPNATARESNGVYVLEKVDLHPQLCFKVPWFSGN 360

QY 361 SSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMMHATFSAAWSLPLCGDITLVPVYTV 420

Db 361 SSHVECPHOTGSLTSWNVSMDTQAQQLILHFSRMMHATFSAAWSLPLCGDITLVPVYTV 420

QY 421 SQWRSVQFAWKHLICPDYSYRHLGLLLIALLALLTLGLVLLALTCRRPQSGPGPARPV 480

Db 421 SQWRSVQFAWKHLICPDYSYRHLGLLLIALLALLTLGLVLLALTCRRPQSGPGPARPV 480

QY 481 LLLHAADSEAOQRLVGVGALAEALLRAALGGGRDVIIVDLMEGRHVARVGLPWLWAARTVAR 540

Db 481 LLLHAADSEAOQRLVGVGALAEALLRAALGGGRDVIIVDLMEGRHVARVGLPWLWAARTVAR 540

QY 541 EQGTVLLWSGADLRPVGGPDPRAAPLALLHAAAPRLLALLAYFSRLCAKGDIPPLRAL 600

Db 541 EQGTVLLWSGADLRPVGGPDPRAAPLALLHAAAPRLLALLAYFSRLCAKGDIPPLRAL 600

QY 601 PRYRLRLDPLRLRALDARPAEATSWGRLGARQRRQSRLELCSRLREARLADLG 657

Db 601 PRYRLRLDPLRLRALDARPAEATSWGRLGARQRRQSRLELCSRLREARLADLG 657

RESULT 2

AAU04957

ID AAU04957 standard; Protein: 667 AA.

XX AC AAU04957;

XX 24-OCT-2001 (first entry)

DT Human Interleukin 17 receptor, IL-17RH3.

DE

XX Human; Interleukin-17 receptor; IL-17RH3; agonist; antagonist;

KW PR09877; DNA I19502-2789; systemic lupus erythematosus;

KW rheumatoid arthritis; osteoarthritis; diabetes mellitus;

KW allergic disease; asthma; demyelinating disease;

KW degenerative cartilaginous disorder; transplantation associated disease.

XX OS Homo sapiens.

XX Key Location/Qualifiers

FH Peptide 1..23

FT /label= Signal_peptide

FT Protein 24..667

FT /label= Mature_IL_17RH3

FT Region 90..96

FT /note= "N-myristoylation site"

FT Region 104..108

FT /note= "cAMP/GMP-dependent protein kinase phosphorylation site"

FT Modified-site 318..322

FT /note= "Asn is N-glycosylated"

FT Region 322..329

FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 347..351

FT /note= "Asn is N-glycosylated"

FT Region 358..364

FT /note= "N-myristoylation site"

FT Modified-site 364..368

FT /note= "Asn is N-glycosylated"

FT Region 453..462

FT /note= "Eukaryotic cobalamin-binding protein motif"

FT Domain 455..472

FT /note= "Transmembrane domain"

FT Region 470..476

FT /note= "N-myristoylation site"

FT Region 482..486

FT /note= "Glycosaminoglycan attachment site"

FT Region 645..649

FT /note= "cAMP/GMP-dependent protein kinase phosphorylation site"

XX WO200146420-A2.

XX 28-JUN-2001.

XX 20-DEC-2000; 2000WO-US34956.

XX 23-DEC-1999; 99US-0172096.

PR 30-DEC-1999; 99WO-US31274.

PR 11-JAN-2000; 2000US-0175481.

PR 18-FEB-2000; 2000WO-US04341.

PR 02-MAR-2000; 2000WO-US05841.

PR 21-MAR-2000; 2000US-0191007.

PR 21-MAR-2000; 2000WO-US07532.

PR 02-JUN-2000; 2000WO-US15264.

PR 22-JUN-2000; 2000US-0213087.

PR 22-AUG-2000; 2000US-0644848.

PR 24-AUG-2000; 2000WO-US23328.

PR 24-OCT-2000; 2000US-0242837.

PR 10-NOV-2000; 2000US-030873.

PR 28-NOV-2000; 2000US-0253646.

PR 01-DEC-2000; 2000WO-US32678.

XX (GETH) GENENTECH INC.

XX Chen J, Filvaroff E, Fong S, Goddard A, Godowski PJ, Grimaldi CJ;

PI Gurney AL, Li H, Hillan KJ, Tumas D, Van Lookeren M, Vandlen RL;

PI Watanabe CK, Williams PW, Wood WI, Yansura DG;

XX

DR WPI; 2001-451708/48.
 XX N-PSDB; AAS09516.
 PT Novel PRO polypeptides homologous to interleukin-17, useful for the
 PT diagnosis and treatment of immune related disease e.g. rheumatoid
 XX arthritis and diabetes -
 PS Claim 10; Fig 16; 188pp; English.
 XX
 CC The sequence is PRO9877 which is the human Interleukin 17 receptor,
 CC IL-17RH3, encoded by DNA 119502-2789. A composition
 CC containing ant/agonists to the PRO polypeptides or individual components
 CC are useful for treating a mammal with an immune related disease, e.g.
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease, an autoimmune or immune-mediated skin
 CC disease, contact dermatitis, an allergic disease e.g. food
 CC hypersensitivity, asthma, a transplantation associated disease, or a
 CC chronic inflammatory demyelinating polynuropathy. Treating a
 CC degenerative cartilaginous disorder comprises administering a PRO1031 or
 CC PRO1122 polypeptide agonist, or antagonist to the mammal. Numerous
 CC examples of the diseases and disorders are given in the specification.
 XX
 SQ Sequence 667 AA;

Query Match 77.2%; Score 2711; DB 22; Length 667;
 Best Local Similarity 77.5%; Pred. No. 2e-239;
 Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSSRLAALLPLLLIVIDLSDSAGIGRHLPHNTRCPPLASHTEVLPISLAAPGGSP 60
 DB 1 MGSSRLAALLPLLLIVIDLSDSAGIGRHLPHNTRCPPLASHTEVLPISLAAPGGSP 60
 QY 61 QSLGVCESGTPVAVCASTCCQVAFNGASSTWCNPKSLPHSSIGDTQCOHLL---- 116
 DB 46 -----DSFTGSSAYPCRTWAL--FSTKPMW--VRVWCHSR--CLCQHLLSGGS 89
 QY 117 ---RGSCVLVTCRLRAITF-----PSPQTS--PTRDFALKGNLRIQRHGKVPDP 163
 DB 90 GLQGLFHLVQKSKSTFFRYRHKMPAPAQRKLLPRRHLSKSHIIPS-----PD 144
 QY 164 WTHGM-----EVGTGYNRWVQLSGGPEFSDLLPEARAIIVTISSGPEVSRL 213
 DB 145 ISHKLRSKRTPQSDPETWESLPRLDQSQRHGGPEFSDLLPEARAIIVTISSGPEVSRL 204
 QY 214 CHQWALECEELSSPYDQKIVSGGHTVELPYEFLPCLCIEASYLQEDTVRRKKCPQSQW 273
 DB 205 CHQWALECEELSSPYDQKIVSGGHTVELPYEFLPCLCIEASYLQEDTVRRKKCPQSQW 264
 QY 274 PEAYGSDFWKSVHFTDYQHTQVMYVNTLTLCPLKLEALCORHWHHTLCKDLNPATARES 333
 DB 265 PEAYGSDFWKSVHFTDYQHTQVMYVNTLTLCPLKLEALCORHWHHTLCKDLNPATARES 324
 QY 334 DGWVLEKVDLHPOLCFKVPWFSGNSSHVECPHQTSITSNVNSMDTQAQQLILHFS 393
 DB 325 DGWVLEKVDLHPOLCFK----FSFGNSSHVECPHQTSITSNVNSMDTQAQQLILHFS 380
 QY 394 RMHATFSAANSLPGLGDTLVPPVYVTSQ-----VWRSQVQF 430
 DB 381 RMHATFSAANSLPGLGDTLVPPVYVTSQARSSPSVSLDLIIPFLPGCCVLVWRSQVQF 440
 QY 431 AKWHLCPDVSRYHLGLIILALLLTLGLVWLTALTCRRPQSGPGPARPVLLLHAADSEA 490
 DB 441 AKWHLCPDVSRYHLGLIILALLLTLGLVWLTALTCRRPQSGPGPARPVLLLHAADSEA 500
 QY 491 QRLVGLAELLRAALGGGRDVIDLWEGRHVARVGLPWLWAARTVAREQGTVLLWS 550
 DB 501 QRLVGLAELLRAALGGGRDVIDLWEGRHVARVGLPWLWAARTVAREQGTVLLWS 560
 QY 551 GADLRPVSGDPRAAPLLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPYRLLRDLP 610

Db 561 GADLRPVSGDPRAAPLLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPYRLLRDLP 620
 QY 611 RLLRALDARPAEATSWGRLGARORRQSRLELCSRLEREARLADLG 657
 DB 621 RLLRALDARPAEATSWGRLGARORRQSRLELCSRLEREARLADLG 667
 RESULT 3
 AAU83601
 ID AAU83601 standard; Protein; 667 AA.
 AC AAU83601;
 XX
 DT 08-MAY-2002 (first entry)
 XX
 DE Human PRO protein, Seq ID No 20.
 XX
 KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 OS Homo sapiens.
 XX
 PN WO200208288-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX
 PR 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2000WO-US34956.
 PR 10-MAY-2001; 2001WO-US06520.
 PR 25-MAY-2001; 2001US-0854280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
 XX
 DR WPI; 2002-172001/22.
 DR N-PSDB; ABK33545.
 XX
 PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11; Figure 20; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung

CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.

XX Sequence 667 AA;

Query Match 77.2%; Score 2711; DB 23; Length 667;
 Best Local Similarity 77.5%; Pred. No. 2e-239;
 Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTCPPLASHTVEPLISLAAPGPGSP 60
 DB 1 MGSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTCPPLASHTD----- 45
 QY 61 QSLGVCESGTPVAVCASICQVAVNGASSTWCNPKSLPHSSSIGDTRCOHLL---- 116
 DB 46 -----DSFTGSSAVIPCKTWWAL--FSTKPCW---VRVHCSSR---CLCQHLLSGGS 89
 QY 117 ---RGSCCLVVTCLRRATIF-----PSPQTS--PTRDFALKGNPLRIORHGKVFDP 163
 DB 90 GLQGLFHLVQKSKSTEFYRHKMPAPAKKLLPRHLSEKSHHITSIPS-----PD 144
 QY 164 WTHKGM-----EVGTGYRRWVQLSGGPEFDFLLPEARAIKVTISSGPEVSRL 213
 DB 145 ISHGLSKRTQSPDPTWESLPRLDSQRHGPEFDFLLPEARAIKVTISSGPEVSRL 204
 QY 214 CHQWALECELSSPYDQKIVSGHTVELPEYELLPCICEASYLQEDTVRRKKCFQSW 273
 DB 205 CHQWALECELSSPYDQKIVSGHTVELPEYELLPCICEASYLQEDTVRRKKCFQSW 264
 QY 274 PEAYGDFWKSVDYDYSQHTQVMYALTLRCPKLEALCQRHDWHTLCKDLPNATARES 333
 DB 265 PEAYGDFWKSVDYDYSQHTQVMYALTLRCPKLEALCQRHDWHTLCKDLPNATARES 324
 QY 334 DGWVLEKVDLHPOLCFKQVWFSGNSHVCEPHQTSNWSMDTQAQQLILHFSS 393
 DB 325 DGWVLEKVDLHPOLCFK-----FSGNSHVCEPHQTSNWSMDTQAQQLILHFSS 380
 QY 394 RMHATFSAWSLPGIGQDTLPPVYTVSQ-----VWRSVDQF 430
 DB 381 RMHATFSAWSLPGIGQDTLPPVYTVSQARGSSPVSLLDILPLRPGCCVWVRSVDQF 440
 QY 431 AWKHLCPDVSYRHGLLILALLLTLGVLVLTALTCRRPQSGPGPARVLLHAADSEA 490
 DB 441 AWKHLCPDVSYRHGLLILALLLTLGVLVLTALTCRRPQSGPGPARVLLHAADSEA 500
 QY 491 QRRVLGALAEALLRAALGGGRVIVDLMEGRHVARVGLPWLWARTVAREQGVLLWS 550
 DB 501 QRRVLGALAEALLRAALGGGRVIVDLMEGRHVARVGLPWLWARTVAREQGVLLWS 560
 QY 551 GADLRPVSGPDPRAAPLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 610
 DB 561 GADLRPVSGPDPRAAPLALLHAAPRPLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 620
 QY 611 RLLRALDARPAEATSWGRGLGARQRQRSLRLEICSRLEAREARLADLG 657
 DB 621 RLLRALDARPAEATSWGRGLGARQRQRSLRLEICSRLEAREARLADLG 667

RESULT 4
 ID AAY76048
 XX AAY76048 standard; Protein; 617 AA.
 AC AAY76048;
 XX

DT 27-MAR-2000 (first entry)
 XX Murine skin cell protein, SEQ ID NO:303.
 DE
 XX Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 KW secreted; transmembrane; inflammation; cancer; neurological disease;
 KW angiogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulvury.
 XX
 OS Mus sp.
 XX WO9955865-A1.
 PN 04-NOV-1999.
 XX 29-APR-1999; 99WO-NZ00051.
 XX 29-APR-1998; 98US-0069726.
 PR 09-NOV-1998; 98US-0188930.
 XX (GENE-) GENESIS RES & DEV CORP LTD.
 PA Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 XX WPI; 2000-072177/06.
 XX N-PSDB; AAZ61753.
 DR Novel polynucleotides useful for the treatment of various conditions
 XX including wounds and cancer -
 PT Claim 4; Page 179-180; 235pp; English.

CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin. Keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
 CC by cDNA sequences derived from several mouse, rat or human skin cell
 CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
 CC AAY76119 are proteins with an N-terminal signal sequence, indicating
 CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
 CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
 CC putative transmembrane domains.

XX Sequence 617 AA;

Query Match 52.1%; Score 1831.5; DB 21; Length 617;
 Best Local Similarity 57.7%; Pred. No. 8.4e-159;
 Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY 1 MGSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTCPPLASHTVEPLISLAAPGPGSP 60
 DB 1 MGSRLAALLPLLLIVIDLSDSAGIGFRHLPHWNTCPPLASHTD----- 45
 QY 61 QSLGVCESGTPVAVCASICQVAVNGASSTWCNPKSLPHSSSIGDTRC---QHLL 116
 DB 46 KRFAGLQWGFPLD-----VRKSKPPKFEDYWRHRTPASQRL 85
 QY 117 RGSCCLVVTCLRRATIFPSPQTSPTDFALKGNPLRIORHGKVFDPDTHKMGVEVTGN 176
 DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQSAAGREHLPEAGS--- 131
 QY 177 RRVQVLSGGPEFDFLLPEARAIKVTISSGPEVSRLCHOWALECELSPPYDQKIVSG 236
 DB 132 ----QKGGPEFDFLLPEVQAVRVITIPAGPKASVRLCIOWALECEDLSPPFTQKIVSG 187

CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.

QY 237 GHTVELPYEFLPCLCIEASYLQEDTVRRKCPQSWPEAYGDFWKSVFHFTDYSQHTQM 296
DQ 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKCPQSWPEAYGDFWQSFRTFTDYSQHNQM 247
QY 297 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLEKVDLHPOLCFKVPWF 356
DQ 248 VMALTRCPLKLEASLCWRQDPLTPCETLPNATAQESGWIENVDLHPOLCFK- ---F 303
QY 357 SFGNSHVECPHOTGSLTWNVSMQTAQOQLLHFSRHHATFSAWSLPGIGDPTLVP 416
DQ 304 SFENSHVECPHQSGLSPWTSMDTQAOQLTHFSRTYATFSAWSLPGIGDPTLVP 363
QY 417 VYTVSQ- ---VWRSVQFAWKHLLCPDVSRYHLGLLILALL 453
DQ 364 VYSISQTSQSVPTLTLIIFLRQENCILVWRSVDFHFAWKHVLCDPDPYPTQLLRSL- 422
QY 454 ALLTLGVVLTALTCRRPQSGPGPARPVLLHAADEAQRRLVGALELRLALGGRDVI 513
DQ 423 - ---GSGRTRPVLLHAADEAQRRLVGALELRLALGGRDVI 463
QY 514 VDLWEGHVARVGLPWLWAARTVAREQGTVLLHNSGADLRPVSGDPPRAAPLALLHA 573
DQ 464 VDLWEGHVARVGLPWLWAARTVAREQGTVLLHNSGADLRPVSGDPPRAAPLALLHA 523
QY 574 APRPLLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRGAR 633
DQ 524 APRP-LLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRGAR 582
QY 634 QRRQSRLELCSRLEREAR 652
DQ 583 RCLKNRLEQCHLLEAAK 601

RESULT 5
AAB55987
ID AAB55987 standard; Protein; 617 AA.
AC AAB55987;
DT 08-MAR-2001 (first entry)
DE Skin cell protein, SEQ ID NO: 303.
KW Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW neotropic; neuroprotective; vulnary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease.
OS Mus sp.
PN WO200069884-A2.
XX 23-NOV-2000.
XX 15-MAY-2000; 2000WO-NZ00075.
XX 14-MAY-1999; 99US-0312283.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX WPI: 2001-007495/01.
XX N-PSDB; AAC99686.
XX New isolated polynucleotide used in the identification of genetic
XX disorders and encoding polypeptides used for treating inflammatory
XX disease, cancer and neurological diseases -
XX Claim 4; Page 244-245; 352pp; English.
XX The present sequence is a polypeptide which is expressed in

CC Query Match 52.1%; Score 1831.5; DB 22; Length 617;
CC Best Local Similarity 57.7%; Pred. No. 8.4e-159;
CC Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;
QY 1 MGSSRLAALLPPLLIVIDLSDSAGIGRHLPHWNTCPCLASHTEVLPISLAAPGGSPSP 60
DQ 1 MGSPRLAALLPPLLIVIDLSDSAGIGRHLPHWNTCPCLASHTEVLPISLAAPGGSPSP 60
QY 61 QSLGVCESGTPVAVCASICQVAVENGASSTSWCRNPKSLPHSSSISGDTTC- ---QHLL 116
DQ 46 KRFAGLQWGFLL- ---VRKSKPPKFEEDYWRHRTFASQRL 85
QY 117 RGSCCLVVTCLRAITFPSPQSPTRDFALKGNLRIORHGKVFDPWTHKGMEVGTGN 176
DQ 86 LGSPLSEESH- ---ISIPSS- ---AISHRGQRTKRAQPSAAEGREHLPEAGS- --- 131
QY 177 RRVQLSGGPEFSDLLPEARAIKRTISSGPEVSVRLCHOWALECELSPPYDQKIVSG 236
DQ 132 - ---QKCGPEFSDLLPEQAVRVTPAGKASVRLCYQWALECEDLSPEDTQKIVSG 187
QY 237 GHTVELPYEFLPCLCIEASYLQEDTVRRKCPQSWPEAYGDFWKSVFHFTDYSQHTQM 296
DQ 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKCPQSWPEAYGDFWQSFRTFTDYSQHNQM 247
QY 297 VMALTRCPLKLEAALCORHWHITCKDLPNATARESDGWYLEKVDLHPOLCFKVPWF 356
DQ 248 VMALTRCPLKLEASLCWRQDPLTPCETLPNATAQESGWIENVDLHPOLCFK- ---F 303
QY 357 SFGNSHVECPHOTGSLTWNVSMQTAQOQLLHFSRHHATFSAWSLPGIGDPTLVP 416
DQ 304 SFENSHVECPHQSGLSPWTSMDTQAOQLTHFSRTYATFSAWSLPGIGDPTLVP 363
QY 417 VYTVSQ- ---VWRSVQFAWKHLLCPDVSRYHLGLLILALL 453
DQ 364 VYSISQTSQSVPTLTLIIFLRQENCILVWRSVDFHFAWKHVLCDPDPYPTQLLRSL- 422
QY 454 ALLTLGVVLTALTCRRPQSGPGPARPVLLHAADEAQRRLVGALELRLALGGRDVI 513
DQ 423 - ---GSGRTRPVLLHAADEAQRRLVGALELRLALGGRDVI 463
QY 514 VDLWEGHVARVGLPWLWAARTVAREQGTVLLHNSGADLRPVSGDPPRAAPLALLHA 573
DQ 464 VDLWEGHVARVGLPWLWAARTVAREQGTVLLHNSGADLRPVSGDPPRAAPLALLHA 523
QY 574 APRPLLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRGAR 633
DQ 524 APRP-LLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRGAR 582
QY 634 QRRQSRLELCSRLEREAR 652
DQ 583 RCLKNRLEQCHLLEAAK 601

RESULT 6
AAB72187
ID ABB72187 standard; Protein; 617 AA.
XX ABB72187;
AC ABB72187;
XX 04-APR-2002 (first entry)
XX

DE Murine protein isolated from skin cells SEQ ID NO: 303.

XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect; developmental defect; inflammatory disease; dermatological; vulnary;

KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

XX Mus sp.

XX WO200190357-A1.

PN 29-NOV-2001.

XX 24-MAY-2001; 2001WO-NZ00099.

XX 24-MAY-2000; 2000US-206650P.

PR 25-JUL-2000; 2000US-221232P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PA Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD; WPI; 2002-122020/16.

XX New polynucleotides and polypeptides encoded by the polynucleotides isolated from skin cells, useful for treating skin wounds, cancers, growth and developmental defects, inflammatory diseases, or for modulating immune responses -

XX Example 2; Page 200-201; 466pp; English.

XX The present invention provides the protein and coding sequences of cDNAs isolated from human, murine and rat skin cell libraries. The sequences can be used in the development of therapeutic agents useful in the treatment of skin diseases, including skin wounds, cancer, growth defects, developmental defects and inflammatory diseases. The proteins have important roles in the induction of hair growth, cell proliferation and cell-cell interaction, in maintaining tissue integrity, in wound healing and in modulating immune responses. The present sequence is a polypeptide of the invention.

XX SQ Sequence 617 AA;

Query Match 52.1%; Score 1831.5; DB 23; Length 617;

Best Local Similarity 57.7%; Pred. No. 8.4e-159;

Matches 392; Conservative 49; Mismatches 133; Indels 105; Gaps 10;

QY 1 MGSSRLAALLPPLLIVLSDSAGIGFRLPHWNTCRPLASHTEVLPISLAAPGSPSP 60

DB 1 MGSPRLAALLLPLLLIGLAVSARVACPLRSWTSHCLLAYRVD----- 45

QY 61 QSLGVCEGTVPACASICQVAVNGASSTSWCRNPKSLPHSSSIGDTRC---QHLL 116

DB 46 KRPAQLQWGFPL-----VKSKSPKFDYWRHRTFASQFKL 85

QY 117 RGSCLVVTCLRRATFPSPQTSPTDFALKGNLRIRHGKVFDPDTHKMEVGTGYN 176

DB 86 LGSPLSESHR--ISIPSS-----AISRGQRTKRAQPSAAEGREHLPEAGS--- 131

QY 177 RRVQLSGGFEDLLPEARATRVISSGPEVSVRLCHQWALECELSPPYDVOKIVSS 236

DB 132 ----QKGGPEFDFLLPEQAVRVTPAGPKASVRLCQWALECELSPPDTPQIVSG 187

QY 237 GHTVELPEFLLPCLCEASYLOEDTVRRKKCPFSQWPEAYGSDFKWSVHFTDYSOHTQM 296

DB 188 GHTVDLPYELLFCMCEASYLOEDTVRRKKCPFSQWPEAYGSDFKWSVHFTDYSOHTQM 247

QY 297 VMALTLRCLPLKLAALCQRHWHITCKDLPNATARSQWYVLEKVDLHPQLCFKVPQWF 356

DB 248 VMALTLRCLPLKLEASLCWRQDPLTPCETLPNATAQSEGWYILENVDLHPQLCFK----F 303

QY 357 SFGNSSHVECPHQGTSTNNVSMDTQAQOLILHFSRHMATFSAWSLPLGQDTLVPP 416

DB 304 SFNSSHVECPHOSGLSPSVTWSMDTQAQQLTLHFSRKYATFSAWSDFGLGDTFMP 363

QY 417 VYTVSQ-----VWRSQVQFAWKHLCPDVSYRHLGLLALL 453

DB 364 VYSISOTQSGVPVTLDLIIFFLRQENCILVWRSDFVFAWKHLCPDPAVPTQLLRSL- 422

QY 454 ALLTLGVVIALTCRRPQSGPGPARPVLLLHAADSAQRRLVGALAEILRAALGGGRDVI 513

DB 423 -----GSGTRPVLVLLHAADSAQRRLVGALAEILRTALGGGRDVI 463

QY 514 VDLWEGHVARVGPPLWAAARTVAREQGTVLLWSGADLRPVSGPDPAAPFLALLHA 573

DB 464 VDLWEGTHVARIIGLPLWAAERVAREQGTVLLWNCACGPSTACSGDQQAASLRTLLCA 523

QY 574 APRPLLLAYFSRLCAKGDIPPLRALPRYLRLDLPRLRALDARPFAPATSWGRIGAR 633

DB 524 APRP-LLAYFSRLCAKGDIPPLRALPRYLRLDLPRLRALDAPATLASSWSHLGAK 582

QY 634 ORRQSRLELCSRLEREAAAR 652

DB 583 RCLKNRLEQCHLLEAAK 601

RESULT 7

AAU83238

ID AAU83238 standard; Protein; 226 AA.

XX AAU83238;

XX 08-MAY-2002 (first entry)

XX Novel secreted protein Z935805G4P.

XX Protein secretion; mammalian secreted polypeptide; MSP.

XX Homo sapiens.

XX WO200202621-A2.

XX 10-JAN-2002.

XX 28-JUN-2001; 2001WO-US20638.

XX 30-JUN-2000; 2000US-215446P.

XX (ZYMO) ZYMOGENETICS INC.

XX Sheppard PO, Presnell SR;

XX WPI; 2002-147999/19.

XX N-PSDB; ABK33153.

XX Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits

XX Claim 12; Page 396-397; 397pp; English.

XX The invention describes an isolated mammalian secreted polypeptide (MSP) (I). (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide, to screen for cell metabolism effecting receptors, for identifying new target receptors and drug design, for identifying, for protein purification, for determining the weight of expressed MSP polypeptides as a ratio to total protein expressed, for identifying peptide cleavage sites, for coupling amino and carboxy terminal tags, for amino acid sequence analysis, for monitoring biological activities of the protein in vitro and in vivo, and to teach analytical skills and as reagents for the study of cells, receptors, and other binding molecules. The polynucleotide is useful for radiation hybrid mapping, and somatic cell genetic technique developed for constructing high-resolution, contiguous maps of mammalian chromosomes. Reagents disclosed in the

CC invention may be used to detect metabolic abnormalities characterised by
CC over or under production of the protein. This is the amino acid sequence
CC of a mammalian secreted polypeptide, described in the method of the
CC invention.

SQ Sequence 226 AA;
Query Match 31.5%; Score 1108; DB 23; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.3e-93;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 440 VSYRHGLLILALLLTLGLVVLALTCRRPQSGPGPARPVLLHHAADSEARQLVGLA 499
Db VSYRHGLLILALLLTLGLVVLALTCRRPQSGPGPARPVLLHHAADSEARQLVGLA 68
QY 500 ELLRAALGGGRDVIIVDLNMGHVARVGPPLPWLWAARTVAREQGVLLWLGADLRPVSG 559
Db ELLRAALGGGRDVIIVDLNMGHVARVGPPLPWLWAARTVAREQGVLLWLGADLRPVSG 128
QY 560 PDPAAPLALHAAAPRPLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLRLALDAR 619
Db PDPAAPLALHAAAPRPLLLAYFSRLCAKGDIPPLRALPRYRLRLDLPRLRLALDAR 188
QY 620 PFAEATSWGRGARORRSRLCRLEREARLADLG 657
Db PFAEATSWGRGARORRSRLCRLEREARLADLG 226

RESULT 8
AA75947
ID AA75947 standard; Protein; 330 AA.
XX
AC AA75947;
XX
DT 27-MAR-2000 (first entry)
XX
DE Murine skin cell secreted protein, SEQ ID NO:125.
XX
KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW secreted; transmembrane; inflammation; cancer; neurological disease;
KW angiogenesis; tumour vascularisation; growth disorder;
KW developmental disorder; skin wound; hair follicle disorder;
KW anti-inflammatory; cytostatic; neuroprotective; vulnery.
XX
OS Mus sp.
XX
PN W09955865-A1.
XX
PD 04-NOV-1999.
XX
PF 29-APR-1999; 99WO-NZ00051.
XX
PR 29-APR-1998; 98US-0069726.
PR 09-NOV-1998; 98US-0188930.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
DR WPI: 2000-072177/06.
DR N-PSDB: AA261611.
XX
PT Novel polynucleotides useful for the treatment of various conditions
PT including wounds and cancer -
PS
PS Claim 4; Page 102-103; 235pp; English.
XX
CC The invention relates to novel nucleic acid sequences derived from rat
CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
CC cells. Polypeptides of the invention may be used to treat inflammation,
CC cancer and neurological diseases. The proteins may be used to stimulate

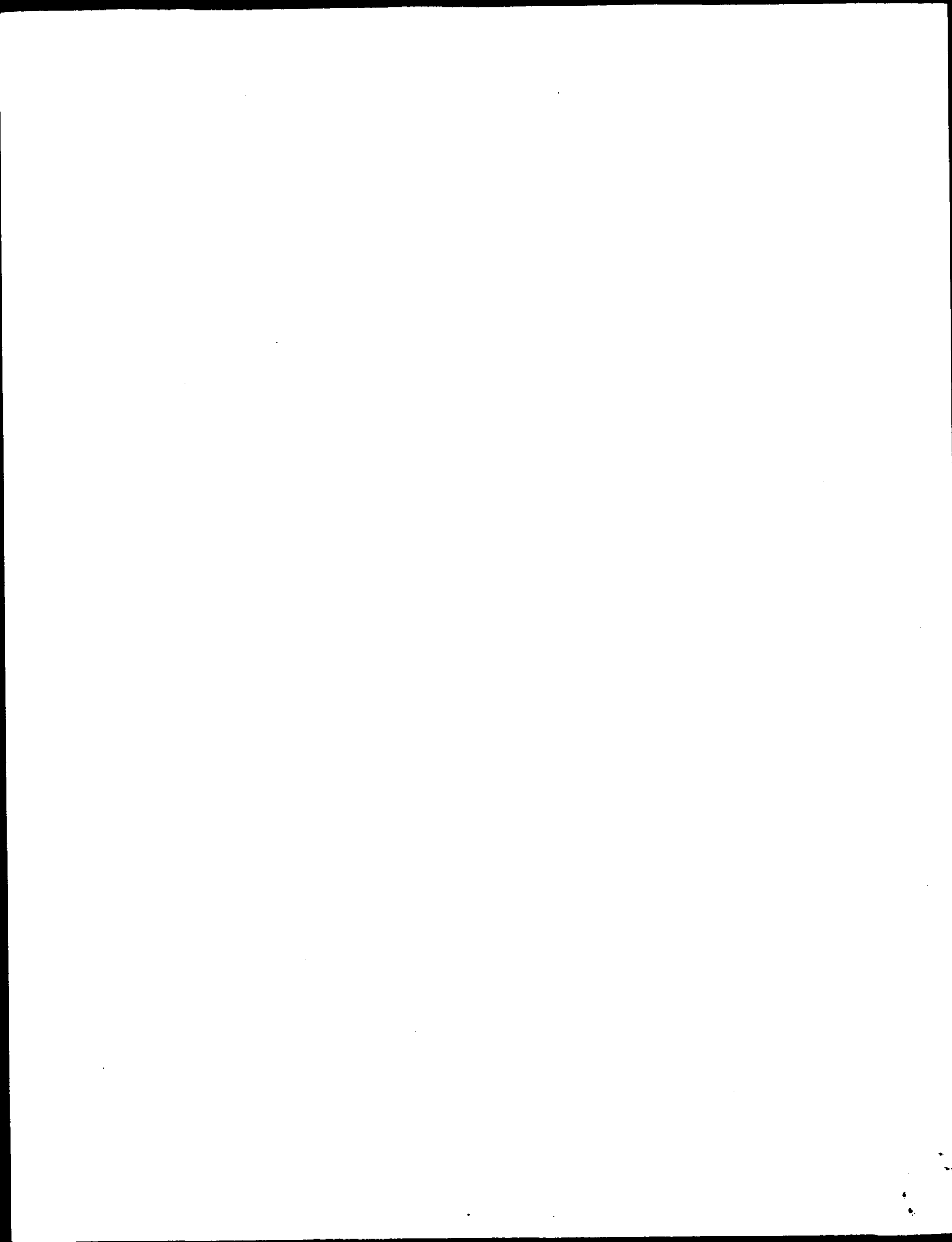
CC the growth and motility of keratinocytes, to inhibit the growth of
CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
CC modulate skin inflammation, to modulate epithelial cell growth and to
CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
CC to treat growth and developmental defects, skin wounds and hair follicle
CC disorders. Sequences AAY75942-Y76123 represent polypeptides encoded
CC by cDNA sequences derived from several mouse, rat or human skin cell
CC types. Sequences AAY75942-Y75947, AAY76020-Y76021, AAY76094-Y76104 and
CC AAY76119 are proteins with an N-terminal signal sequence, indicating
CC that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071,
CC AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more
CC putative transmembrane domains.
XX
SQ Sequence 330 AA;
Query Match 27.0%; Score 948.5; DB 21; Length 330;
Best Local Similarity 53.2%; Pred. No. 3.2e-78;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;
QY 1 MGSRLAALLPLLLIIVLSDSAGIGRHLPHWNTCRPLASHTVLPISLAAPGGPSSP 60
Db 1 MGSRLAALLPLLLIIVLSDSAGIGRHLPHWNTCRPLASHTVLPISLAAPGGPSSP 60
QY 61 QSLGVCESTVPVAVCASICCOVAVENGASSTWCRNPKSLPHSSISGDTGTRC----QHLL 116
Db QSLGVCESTVPVAVCASICCOVAVENGASSTWCRNPKSLPHSSISGDTGTRC----QHLL 116
QY 117 RGSCLVVTCLRRAITFPSPPTSPTRDFALKGNLRIQRHKGKVFDPWTHKGMEVGTGN 176
Db RGSCLVVTCLRRAITFPSPPTSPTRDFALKGNLRIQRHKGKVFDPWTHKGMEVGTGN 176
QY 177 RRVQLSGGPEFDFLLPEARAIRVTISSGPEVSVRLCHQWALECELSPPYDVQKIVSG 236
Db RRVQLSGGPEFDFLLPEARAIRVTISSGPEVSVRLCHQWALECELSPPYDVQKIVSG 236
QY 132 ----QKGGSGPEFDFLLPEVAVRTIPAGKASVRLCYQWALECEDLSPPFTQKIVSG 187
Db ----QKGGSGPEFDFLLPEVAVRTIPAGKASVRLCYQWALECEDLSPPFTQKIVSG 187
QY 237 GHTVELPYEFLPCLCIEASYLOEDTVRRKKCPFSWPEAYGSDFWKSVHFTDYSOHTQM 296
Db GHTVELPYEFLPCLCIEASYLOEDTVRRKKCPFSWPEAYGSDFWKSVHFTDYSOHTQM 296
QY 188 GHIVDLPYELLPCMCIEASYLOEDTVRRKKCPFSWPEAYGSDFWKSVHFTDYSOHTQM 247
Db GHIVDLPYELLPCMCIEASYLOEDTVRRKKCPFSWPEAYGSDFWKSVHFTDYSOHTQM 247
QY 297 VMALTURCPKLKLAALCQRHWHITLCKDLNPATARESDGWYVLEKVDLHPQLCFKVPWF 356
Db VMALTURCPKLKLAALCQRHWHITLCKDLNPATARESDGWYVLEKVDLHPQLCFKVPWF 356
QY 248 VMALTURCPKLKLAALCQRHWHITLCKDLNPATARESDGWYVLEKVDLHPQLCFK 303
Db VMALTURCPKLKLAALCQRHWHITLCKDLNPATARESDGWYVLEKVDLHPQLCFK 303
QY 357 SFGNSSHVCEPHOTGSILTSWNVSMDTQ 383
Db SFGNSSHVCEPHOTGSILTSWNVSMDTQ 383
QY 304 SFENSHVCEPHOTGSILTSWNVSMDTQ 330
Db SFENSHVCEPHOTGSILTSWNVSMDTQ 330
RESULT 9
AAB55886
ID AAB55886 standard; Protein; 330 AA.
XX
AC AAB55886;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell protein, SEQ ID NO: 125.
XX
KW Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW neurotropic; neuroprotective; vulnery; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease.
XX
OS Mus sp.
XX
PN W0200069884-A2.
XX
PD 23-NOV-2000.
XX
PF 15-MAY-2000; 2000WO-NZ00075.
XX
PR 14-MAY-1999; 99US-0312283.
XX

PA (GENE-) GENESIS RES & DEV CORP LTD.
XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX WPI; 2001-007495/01.
XX
XX New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
XX
XX
XX Claim 4; Page 136-137; 352pp; English.
XX
XX The present sequence is a polypeptide which is expressed in
CC mammalian skin cells. The polypeptide is useful for stimulating
CC keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC tumours, modulating skin inflammation, stimulating the growth of
CC epithelial cells, inhibiting the binding of human immunodeficiency virus
CC (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC neurological diseases. The polynucleotide can be used as a marker, in
CC the identification of genetic disorders, and for the design of
CC oligonucleotides for examining expression patterns.
XX
XX Sequence 330 AA;
SQ
Query Match 27.0%; Score 948.5; DB 22; Length 330;
Best Local Similarity 53.2%; Pred. No. 3.2e-78;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;
QY 1 MGSSRLAALLPLLLIIVLSDSAGIGFRHLPHWNTCRPLASHTEVLPISLAAPGGPSP 60
DB 1 MGSPRLAALLSLPLLLIGLAVSARVACPCLSRWSHCLLAYRVD----- 45
QY 61 QSLGVCESTVPVAVCASICQVAVNGASSTWCNRPKSLPHSSSIGDTRC----QHLL 116
DB 46 KRFAGLQWGFPLL-----VRKSKPPKFEDYWRHRTPASFORKL 85
QY 117 RGSCLVVTCLRRATTFPPSPPTSDTRDFALKGNLRIQRHGKVPDWTGMEVGTGYN 176
DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAGREHLPEAGS--- 131
QY 177 RRVQLSGGPEFSDLLPEARAIKRVTISSGPEVSVRLCHQWALECEELSSPDYQKIVSG 236
DB 132 ----QKCGGPEFSDLLPEVQAVRVTIPAGPKASVRLCYQWALECEDLSSPDFTQKIVSG 187
QY 237 GHTVLPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGDFWKSVFHTDYSHQTM 296
DB 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCPQSWPEAYGDFWQSIIRFTDYSQHNQM 247
QY 297 VMALTLRCPCLKLEAALCQRHDWHTLCKDLPNATARESOGWYVLEKVDLHPQLCFKVPWF 356
DB 248 VMALTLRCPCLKLEASLCWRQDPLTPCETLPNATAQESGWYILENVDLHPQLCFK----F 303
QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQ 383
DB 304 SFENSSHVECPHQSGSLPSWTVSMDTQ 330
RESULT 10
ABB72086
ID ABB72086 standard; Protein; 330 AA.
XX ABB72086;
XX
XX
XX 04-APR-2002 (first entry)
XX Murine protein isolated from skin cells SEQ ID NO: 125.
XX
XX Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
KW developmental defect; inflammatory disease; dermatological; vulvar; urinary;
KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.
XX
XX Mus sp.
OS

XX WO200190357-A1.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-NZ00099.
XX
XX 24-MAY-2000; 2000US-206650P.
XX
XX 25-JUL-2000; 2000US-221232P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
XX WPI; 2002-122020/16.
XX
XX New polynucleotides and polypeptides encoded by the polynucleotides
PT isolated from skin cells, useful for treating skin wounds, cancers,
PT growth and developmental defects, inflammatory diseases, or for
PT modulating immune responses -
XX
XX Example 2; Page 118-119; 466pp; English.
XX
XX The present invention provides the protein and coding sequences of cDNAs
CC isolated from human, murine and rat skin cell libraries. The sequences
CC can be used in the development of therapeutic agents useful in the
CC treatment of skin diseases, including skin wounds, cancer, growth
CC defects, developmental defects and inflammatory diseases. The proteins
CC have important roles in the induction of hair growth, cell proliferation
CC and cell-cell interaction, in maintaining tissue integrity, in wound
CC healing and in modulating immune responses. The present sequence is a
CC polypeptide of the invention.
XX
XX Sequence 330 AA;
SQ
Query Match 27.0%; Score 948.5; DB 23; Length 330;
Best Local Similarity 53.2%; Pred. No. 3.2e-78;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;
QY 1 MGSSRLAALLPLLLIIVLSDSAGIGFRHLPHWNTCRPLASHTEVLPISLAAPGGPSP 60
DB 1 MGSPRLAALLSLPLLLIGLAVSARVACPCLSRWSHCLLAYRVD----- 45
QY 61 QSLGVCESTVPVAVCASICQVAVNGASSTWCNRPKSLPHSSSIGDTRC----QHLL 116
DB 46 KRFAGLQWGFPLL-----VRKSKPPKFEDYWRHRTPASFORKL 85
QY 117 RGSCLVVTCLRRATTFPPSPPTSDTRDFALKGNLRIQRHGKVPDWTGMEVGTGYN 176
DB 86 LGSPSLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAGREHLPEAGS--- 131
QY 177 RRVQLSGGPEFSDLLPEARAIKRVTISSGPEVSVRLCHQWALECEELSSPDYQKIVSG 236
DB 132 ----QKCGGPEFSDLLPEVQAVRVTIPAGPKASVRLCYQWALECEDLSSPDFTQKIVSG 187
QY 237 GHTVLPYEFLLPCLCIEASYLQEDTVRRKKCPQSWPEAYGDFWKSVFHTDYSHQTM 296
DB 188 GHTVDLPYEFLLPCMCIEASYLQEDTVRRKKCPQSWPEAYGDFWQSIIRFTDYSQHNQM 247
QY 297 VMALTLRCPCLKLEAALCQRHDWHTLCKDLPNATARESOGWYVLEKVDLHPQLCFKVPWF 356
DB 248 VMALTLRCPCLKLEASLCWRQDPLTPCETLPNATAQESGWYILENVDLHPQLCFK----F 303
QY 357 SFGNSSHVECPHOTGSLTSWNVSMDTQ 383
DB 304 SFENSSHVECPHQSGSLPSWTVSMDTQ 330
RESULT 11
ABB08185
ID ABB08185 standard; Protein; 353 AA.
XX
XX ABB08185;
AC

XX 13-FEB-2002 (first entry)
 XX Novel human diagnostic protein #8176.
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72372.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 38544; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 353 AA;
 XX
 Query Match 15.6%; Score 547; DB 22; Length 353;
 Best Local Similarity 99.1%; Pred. No. 2.4e-41;
 Matches 107; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 550 SGADLPVSGDPDRAPIALHAAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLD 609
 DB 246 SGADLPVSGDPDRAPIALHAAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLD 305
 QY 610 PRLLRALDARPAEATSWGRIGARORRORSLCSRLREARLADLG 657
 DB 306 PRLLRALDARPAEATSWGRIGARORRORSLCSRLREARLADLG 353
 RESULT 12
 ABG08183
 ID ABG08183 standard; Protein; 145 AA.

XX ABG08183;
 AC 13-FEB-2002 (first entry)
 XX
 DT Novel human diagnostic protein #8174.
 XX
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 XX
 DR WPI; 2001-639362/73.
 DR N-PSDB; AAS72370.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 PS Claim 20; SEQ ID NO 38542; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 145 AA;
 XX
 Query Match 12.5%; Score 438; DB 22; Length 145;
 Best Local Similarity 100.0%; Pred. No. 6.4e-32;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHNTRCPLASHTEVLPISLAAPGGSSP 60
 DB 1 MGSSRLAALLPLLLIVIDLSDSAGIGFRHLPHNTRCPLASHTEVLPISLAAPGGSSP 60
 QY 61 OSLGVCEGTVPAVCASICCOVAQ 84
 DB 61 OSLGVCEGTVPAVCASICCOVAQ 84
 RESULT 13




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QY 357 SFNSHVECHPQHTGSLTWNVSDMTQAOQLLHFFSSRMHATESAANSLPGLGODTLVPP 416
DB 304 SFNSHVECHPQHTGSLTWNVSDMTQAOQLLHFFSSRMHATESAANSLPGLGODTLVPP 363
QY 417 VYTVSQ-----VWRSVDQFAWKHLPCPDVSYRHLGLLILALL 453
DB 364 VYISQTOGSPVTLDLIIPFLOENCILVWRSVDHFAWKHVLCPDDAPYPTQLLRSL- 422
QY 454 ALLTLGGVVALTCRRPQSGPGPARPVLLLHAADSEARQRLVGAELLLRAALGGGRDVI 513
DB 423 -----GSGRTPVLLLHAADSEARQRLVGAELLLRAALGGGRDVI 463
QY 514 VDLWEGRHVARVCPPLWLAARTVAREQTVLLLWAGDLRPVSGPDPRAAPLILALLHA 573
DB 464 VDLWEGTHVARVGPPLWLAARERVARQTVLLLWAGDLPVSGPDPQAASTLTLCA 523
QY 574 APRPILLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDARPAEATSWGRUGAR 633
DB 524 APRP-LLLAYFSLCAKGDIPPLRALPRYLLRDLPRLLRALDAQPATLASSNSHLGAK 582
QY 634 QRRQSRLELCRLEREAR 652
DB 583 RCLKNRLEQCHLLEAAK 601

RESULT 2
US-09-188-930-125
; Sequence 125, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Steeman, Matthew
; APPLICANT: Onrust, Rene
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods For Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 125
; LENGTH: 330
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-125

Query Match 27.0%; Score 948.5; DB 4; Length 330;
Best Local Similarity 53.2%; Pred. No. 2.3e-87;
Matches 206; Conservative 31; Mismatches 89; Indels 61; Gaps 7;

QY 1 MGSRLAALLPLLLIVLSDSAGICFRHPLHNWTRCPPLASHTVPLISLAAPGPPSP 60
DB 1 MGSPRLAALLPLLLIGLASVAVACPLRSWTSCHLLAYKVD-----45
QY 61 QSLGVCSGTVPAVCASICQVAQVENGASSTWCNRNPKSLPHSSSIGDTRC-----QHLL 116
DB 46 KRFAGLOWGFPL-----VVKSKSPKPFEDYWRHRTPASFORKL 85
QY 117 RGSCLLVVTCRLRAITFPSPQTSPTDRFALKGNLRIQRHGVFPDPTWTHKMEVGTGYN 176
DB 86 LGSPLSESHR--ISIPSS-----AISHRGQRTKRAQPSAAEGREHLPEAGS---131
QY 177 RRVQSLSGGFEFDLLPEARATRVISSGPEVSVRLCHQWALECEELSSPYDVQKIVSG 236
DB 132 -----OKQGGPEFSDLLPEVQAVRVITPAGPKASVRLCYQWALECEELSSPYDVQKIVSG 187
QY 237 GHTVLPYEFLLPCLCIEASYLQEDTVRRKKCPFSQWPAYGSDFWKSVHFDTYSQHTQM 296
DB 188 GHTVDPYEFLLPCMCIEASYLQEDTVRRKKCPFSQWPAYGSDFWKSVHFDTYSQHTQM 247
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QY 297 VMALTRCPLKLEAALCORHWHITLCKLPNATVARESDGWYLVLEKVDLHPQLCFKVPQWF 356
DB 248 VMALTRCPLKLEASLCWRQDPLTPCETLPNATAQSEGWYILENDLHPQLCFK----F 303
QY 357 SFNSHVECHPQHTGSLTWNVSDMTQ 383
DB 304 SFNSHVECHPQSGSLPSWTVSMDTQ 330

RESULT 3
US-08-620-694A-10
; Sequence 10, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694A
; FILING DATE: 21 MARCH 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-620-694A-10

Query Match 3.5%; Score 123; DB 2; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRGSCLLVVTCRLRAITFPSPQTSPTDRFALKGNLRIQRH-----GKVEP---DWT 165
DB 52 VKNSTCLDSDWIHPNLTTPSSPK-----DQIQIHLFAHTQOGDLPFVAHIEWT 99
QY 166 -----HKMEVGT-----CYNRRWVQLSGGPSEFSDLLPEA 196
DB 100 LOTDASILYEGAEULSVLQNTNRLNLCVRFELSKLRHHHRW-----RFTS-----147
QY 197 RAIRVTISGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLLP-----249
DB 148 -----HFVDPQEQYEVTVHH-----LPKIPDGDGNHQSKNFLVDPCEHARM 190
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QY 250 ---CLCIEASYLQEDTV-----RRKKCPFSQSWPEAYGDFWKSVMHFTDYSHQHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFES-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTRNLKGCCHQVQIQPFSSC 290
QY 358 ---FGNSHVCEPHOTGSLTSNWNVMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDT 310
QY 414 VPPVTVSOWMSDQVQFAMKHLCPDVSYRHLGLLIALALLTLLGVVVALTCRRPQSG 473
Db 311 EP-----IPDYNPLWYVWFTIGSILLVGSVIL-----LIVCMWNR--LAG 349
QY 474 PG-----PA-----RPVLLHAADESAQRRLVGAELALLRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPADLIPPLPKPKVWIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVVDLMEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEVESNKKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAAPLIALHAAAPR-----LLLAYFSRLCAKGDIPPLRALPYRL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVYCFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 4

US-09-022-255-10
; Sequence 10, Application US/09022255
; Patent No. 6072033
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072033el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,255
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/620,694
; FILING DATE: 21 MARCH 1996
; APPLICATION NUMBER: USN 08/538,765
; FILING DATE: 7 AUGUST 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USN 08/410,535
; FILING DATE: 23 MARCH 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-255-10

Query Match 3.58; Score 123; DB 3; Length 866;
Best Local Similarity 18.08; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRSGCCLVVTCLRRATFFSPPTSPTRFALPKPNLRIQRH-----GKPEV-----DWT 165
Db 52 VKNSTCLDDSDWHPNLTTPSSPK-----DLQIQLHFAHTQGGDLFPVAHLEWT 99
QY 166 -----HKGMEVGT-----GYNRRWVQLSGGPFESFDLLPEA 196
Db 100 LQTDASILYLEGAELSVLQLTNTERLCVRFEFLSKLRHHRRW-----RFTFS----- 147
QY 197 RAIRVTISSGPEVSVRLCHQWALECEELSSPYDVQKTVSGGHTVLPYEFLLP----- 249
Db 148 ---HFVVDPOQEYEVTVHH-----LPRDIPDGNHOSKNFLVDPCEHARM 190
QY 250 ---CLCIEASYLQEDTV-----RRKKCPFSQSWPEAYGDFWKSVMHFTDYSHQHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTRCPLKLEAALCQRHDWHTLCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFES-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEFHQRSNVTLTRNLKGCCHQVQIQPFSSC 290
QY 358 ---FGNSHVCEPHOTGSLTSNWNVMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDT 310
QY 414 VPPVTVSOWMSDQVQFAMKHLCPDVSYRHLGLLIALALLTLLGVVVALTCRRPQSG 473
Db 311 EP-----IPDYNPLWYVWFTIGSILLVGSVIL-----LIVCMWNR--LAG 349
QY 474 PG-----PA-----RPVLLHAADESAQRRLVGAELALLRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPADLIPPLPKPKVWIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVVDLMEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEVESNKKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAAPLIALHAAAPR-----LLLAYFSRLCAKGDIPPLRALPYRL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVYCFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 5

US-09-022-696-10
; Sequence 10, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle


```

QY 300 LTLRCPLKLEAALCQRHWHHTLCKDLPNATARESDGWYVLEKYVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEPHQRSNVTLLRNKGCRCRHOVQIQPFSSC 290
QY 358 -----FGNSSHVCEPHQTSMTSNVSDMTQAQQLILHFSSRMHATFSAAWSLPGLGQDTL 413
Db 291 LNDCLRHSATVSCPEM----- 310
QY 414 VPPVTVSQVWRSDVQFAWKHLPCPDVSYRHLGLLILALLLTLGLGVVLAALTCRRPQSG 473
Db 311 EP-----IPDYMLVWYFVITGTSILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHHAADSEAOQLVLAELRAALGCG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKPRKWIISADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWLAARTRVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEQATSEAGVMTWVGROKQEMVESNSKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAPLALLHAAPRP-----LALLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDPDLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

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RESULT 7

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US-09-022-253-10
; Sequence 10, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:

```

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)

```

```

; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-10

```

```

Query Match 3.5%; Score 123; DB 3; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

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QY 116 LRGSCLVVTCLRRRAITFPSPQTPTRDFALKGNLRIQRH-----GKYVFP-----DWT 165
Db 52 VKNSTCLDSDSIHPRNLTPSSPK-----DLQIQLHFAHTQQGDLFPVAHIEWT 99
QY 166 -----HKGMEVGT-----CYNRRWVQLSGSPSEFSDLLPEA 196
Db 100 LQTDASILYLGAELSVLQNTNERLCVRFELSKLRHHHRW-----RFTFS----- 147
QY 197 RAIRVTIISGPEVSVYRCHOWALECEELSSPYDVQKIVSGGHTVELPYEFLLP----- 249
Db 148 ---HFVVDPDQEYEVTVHH-----LPKPIPDGDPNHQSKNFLVDPCEHARM 190
QY 250 ---CLCIEASYLQEDTV-----RRKKCPQSWPEAYGDFWKSVFHTDYVSQHTQMVMA 299
Db 191 KVTTCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCQRHWHHTLCKDLPNATARESDGWYVLEKYVDLHPQLCFKVPWFSS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEEPHQRSNVTLLRNKGCRCRHOVQIQPFSSC 290
QY 358 -----FGNSSHVCEPHQTSMTSNVSDMTQAQQLILHFSSRMHATFSAAWSLPGLGQDTL 413
Db 291 LNDCLRHSATVSCPEM----- 310
QY 414 VPPVTVSQVWRSDVQFAWKHLPCPDVSYRHLGLLILALLLTLGLGVVLAALTCRRPQSG 473
Db 311 EP-----IPDYMLVWYFVITGTSILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHHAADSEAOQLVLAELRAALGCG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLPKPRKWIISADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWLAARTRVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEQATSEAGVMTWVGROKQEMVESNSKIIVLCSRGTRAKWQALLGRGAPVRL 467
QY 556 -----PVSGPDPRAPLALLHAAPRP-----LALLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMILPDFKRPACFGTYVVCYFSEVSCDGDVDPDLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

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RESULT 8

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US-09-022-260-10
; Sequence 10, Application US/09022260
; Patent No. 6100235
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6100235el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA

```

```

; ZIP: 98101
; COMPUTER MODEL: FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,260
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
IS-09-022-260-10

```

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> FILING DATE:
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: 08/620,694
> FILING DATE:
> CLASSIFICATION:
> PRIOR APPLICATION DATA:
> APPLICATION NUMBER: US98/410,535
> FILING DATE: 23 MARCH 1995
> CLASSIFICATION:
> ATTORNEY/AGENT INFORMATION:
> NAME: Perkins, Patricia Anne
> REGISTRATION NUMBER: 34,695
> REFERENCE/DOCKET NUMBER: 2617-B
> TELECOMMUNICATION INFORMATION:
> TELEPHONE: (206)587-0430
> TELEFAX: (206)
> INFORMATION FOR SEQ ID NO: 10:
> SEQUENCE CHARACTERISTICS:
> LENGTH: 866 amino acids
> TYPE: amino acid
> TOPOLOGY: linear
> MOLECULE TYPE: protein
> US-09-022-259-10

Query Match 3.5% Score 123; DB 4; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps

QY 116 LRGSCSLVVTCLRAITFPSPQTSPTDFALKCPNLRIQRH-----GKVP-----DWT 165
      ::|||:::|||||:|||||:|||||:|||||:
Db 52 VKNSTCLDSDWIHPNLTTPSPK-----DLQIQLHFAHTQOGLFPVAHIEWT 99
      ::|||:::|||||:|||||:|||||:|||||:
QY 166 -----HKGMVEGT-----GYNRRWQLSGGPESFDLLPEA 196
      ::|||:::|||||:|||||:|||||:|||||:
Db 100 LQTDASILYLGAEALSVLQLTNRLNLCVRFEEFSKLRHHHRW-----RTFS----- 147
      ::|||:::|||||:|||||:|||||:|||||:
QY 197 RAIRVTISGPEFVSRLCHQWALECEEELSSPDYQKIVSGGHTVELPYEFLLP----- 249
      ::|||:::|||||:|||||:|||||:|||||:
Db 148 ---HFVWDQDOEYEVTVIHH-----LPKPTIPDGDPNHQKNTLVDPDCEHARM 196
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QY 250 ---CLCIEASYLQEDTV-----RRKKCPFSQSWPEAYGSDFWKSVHFTDYISOHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCORHWHITCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFWS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEFHQRSNVTLTLRLNKGCCRHQVQIQPFSSC 290
QY 358 ---FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTTP 310
QY 414 VPPVYTVSQWRSQVDFAWKHLCLCPDVSYRHLGLLALLALLTLGLVVALTCRRPQSG 473
Db 311 EP-----IPDYMPLVWYVFIIGISILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHAADEAQRRLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEMVESNSKIIIVLCRGTAKWQALLGRGAPVRL 467
QY 556 -----PVSGDPDPRAPLALLHAAPRP-----LLLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMLPDKRPAFCFTYVVCYFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 10

US-09-022-257-10
; Sequence 10, Application US/09022257
; Patent No. 6197525
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6197525el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,257
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 866 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-257-10

Query Match 3.5%; Score 123; DB 4; Length 866;
Best Local Similarity 18.0%; Pred. No. 0.0029;
Matches 108; Conservative 74; Mismatches 183; Indels 236; Gaps 26;

QY 116 LRGSCCLVVTCLRAITFPSPQPTSPTRFDALGPNLRIQRH-----GKVPF-----DWT 165
Db 52 VKNSTCLDDSWIHPNLTTPSSPK-----DLQIQHFAHTQOQGLFPVAHIEWT 99
QY 166 -----HKGMEVGT-----GYNRRWVQLSGGPEFSFDLLPEA 196
Db 100 LQTDASTLYLEGAELSVLQLNTNERLCVRFEFLSKLRHHHRW-----RFTFS----- 147
QY 197 RAIRVTISSGPEVSVRLCHQWALECELSSPYDQKIVSGGHTVLPYELLP----- 249
Db 148 ---HFVVDPPQEEYEVVHH-----LPKPIPDGDPNHQSKNFLVDPCEHARM 190
QY 250 ---CLCIEASYLQEDTV-----RRKKCPFSQSWPEAYGSDFWKSVHFTDYISOHTQWMA 299
Db 191 KVTTPCMSSGSLWDPNITVETLEAHQLRVSTLWNE-----STHYQILLT 235
QY 300 LTLRCPLKLEAALCORHWHITCKDLPNATARESDGWYVLEKVDLHPQLCFKVPWFWS-- 357
Db 236 ---SFP-HMENHSCFEH-MHHIPAPRPEFHQRSNVTLTLRLNKGCCRHQVQIQPFSSC 290
QY 358 ---FGNSHVECPHOTGSLTSWNVSMDTQAQQLILHFSSRMHATFSAWSLPLGQDTL 413
Db 291 LNDCLRHSATVSCPEM-----PDTTP 310
QY 414 VPPVYTVSQWRSQVDFAWKHLCLCPDVSYRHLGLLALLALLTLGLVVALTCRRPQSG 473
Db 311 EP-----IPDYMPLVWYVFIIGISILLVGSVIL-----LIVCMTWR--LAG 349
QY 474 PG-----PA-----RPVLLHAADEAQRRLVGLAELRAALGGG 509
Db 350 PGSEKYSDDTKYTDGLPAADLIPPLKPRKVMIIYSADHPLYVDVVLKFAQFLLTAC--G 407
QY 510 RDVIVDLWEGRHVARVGPPLWMAARTVAREQGTVLLWS-----GADLR- 555
Db 408 TEVALDLLEEQAISEAGVMTWVGROKQEMVESNSKIIIVLCRGTAKWQALLGRGAPVRL 467
QY 556 -----PVSGDPDPRAPLALLHAAPRP-----LLLAYFSRLCAKGDIPPLRALPRYL 605
Db 468 RCDHGKPVG--DLFTAAMNMLPDKRPAFCFTYVVCYFSEVSCDGDVDFLFGAAPRYPL 525
QY 606 L 606
Db 526 M 526

RESULT 11

US-08-620-694A-2
; Sequence 2, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; STREET: 51 University Street
; CITY: Seattle


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Db 70 -----PSSPKNIYI-----NLVSSTQHGL 90
QY 161 FP-----DWT-----HKGMEVGT-----GYNRRWVQLSGGPE 187
Db 91 VPLVHEWTLOTDSILYLEGAELSVLQNTNRLCVKQFSLMLQHRKRW-----R 143
QY 188 FSDLLPEARARVITSSGPEVSVRLCHQ-----WALECELSPPYDVQ 231
Db 144 FSES-----HFVDPQGEYEVTHLKPDPGDPNHKSKIFVDPDCEDSKMKMTTS 195
QY 232 KIVSG-----GHTVELPYEFLPCLCIEASYLQED--TVRRKKCPQSPWEAYGSDFWKSV 285
Db 196 CVSSGSLWDPNITVE-----TLDQHLRVDFTLWNESTPYQVLLES----- 236
QY 286 HFTDYSQHTQVMYALTLCPLKLEALCORHDWHTLCKDLPNATARESDGHWYVLEKVDLH 345
Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEFH-----QRANVTFTLSKFHWC 276
QY 346 POLCFKVPWFSS-----FGNSHVECPHOTGSLTSWNVSMDSMTQAQQLILHFSSRMHATF 399
Db 277 CHHHVQVQPFSSCLNDCRLRHAVTVPCP----- 304
QY 400 SAANSLPGLGQDTLVP--PVYTVSQWRSDVQPAWKHLPCDPVSYRHLGLL--ILALLALT 457
Db 305 -----VISNTTPKPVADYIPLW-----VYGLITLAILLVGS 337
QY 458 LLGVVLALTCR-----RQSG-----PGPARP--VLLHHAADSEAQRRLV 495
Db 338 VIVLICHTWRLSGADQEKHDDSKINGILPVADLTTPPLRPKRWIVYADHPLYEVV 397
QY 496 GALAEALLRAALGGGRDVIWDLMEGRHVARVGPLMWAARTRVAREQGTVLLWLS---GA 552
Db 398 LKFAQLITAC--GTEVALDLLEEQVISEVGVMTVWSRQKQEMVESNKIILCSRGTA 455
QY 553 DLRPVSG-----PDPRAAPLALLHAAPR-----LALLAYFRLCAKGD 592
Db 456 KWKAILGWAEPVQLRCDHWKPAAGDLFTAAMNMILPDFKRPACFGTVVVCYFSGICSERD 515
QY 593 IPPPLRALPRYRL 606
Db 516 VPDLFNITSRYPLM 529

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RESULT 13

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US-09-022-696-2
; Sequence 2, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037e1 Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:

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; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 864 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-696-2

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Query Match 3.5%; Score 121.5; DB 3; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.0041;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;

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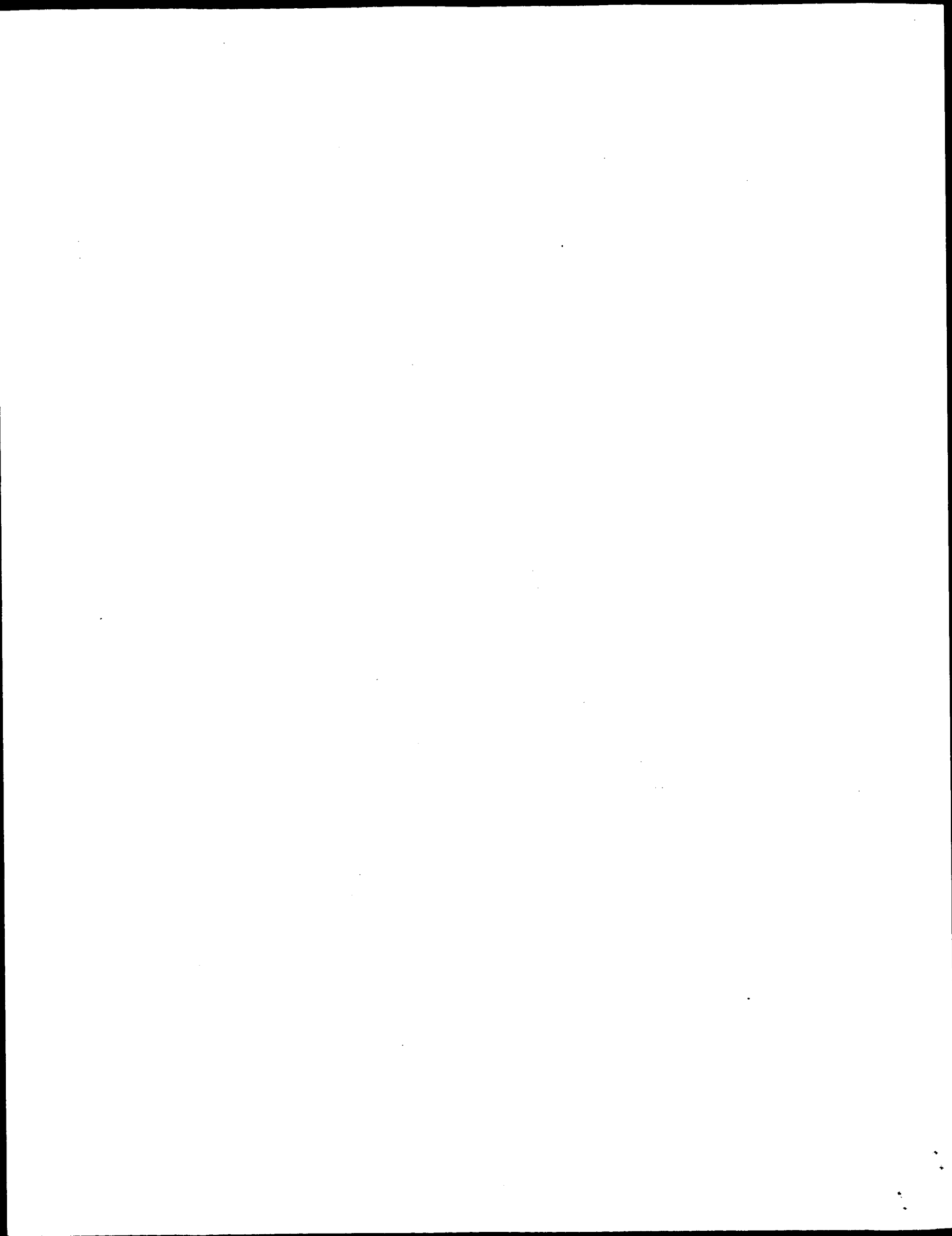
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QY 103 HSSISGTRCQHLRGSCCLVVTCLRRATFPSPOTSPTRDFALKGPNLRQ--RHGKV 160
Db 70 -----PSSPKNIYI-----NLVSSTQHGL 90
QY 161 FP-----DWT-----HKGMEVGT-----GYNRRWVQLSGGPE 187
Db 91 VPLVHEWTLOTDSILYLEGAELSVLQNTNRLCVKQFSLMLQHRKRW-----R 143
QY 188 FSDLLPEARARVITSSGPEVSVRLCHQ-----WALECELSPPYDVQ 231
Db 144 FSES-----HFVDPQGEYEVTHLKPDPGDPNHKSKIFVDPDCEDSKMKMTTS 195
QY 232 KIVSG-----GHTVELPYEFLPCLCIEASYLQED--TVRRKKCPQSPWEAYGSDFWKSV 285
Db 196 CVSSGSLWDPNITVE-----TLDQHLRVDFTLWNESTPYQVLLES----- 236
QY 286 HFTDYSQHTQVMYALTLCPLKLEALCORHDWHTLCKDLPNATARESDGHWYVLEKVDLH 345
Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEFH-----QRANVTFTLSKFHWC 276
QY 346 POLCFKVPWFSS-----FGNSHVECPHOTGSLTSWNVSMDSMTQAQQLILHFSSRMHATF 399
Db 277 CHHHVQVQPFSSCLNDCRLRHAVTVPCP----- 304
QY 400 SAANSLPGLGQDTLVP--PVYTVSQWRSDVQPAWKHLPCDPVSYRHLGLL--ILALLALT 457
Db 305 -----VISNTTPKPVADYIPLW-----VYGLITLAILLVGS 337
QY 458 LLGVVLALTCR-----RQSG-----PGPARP--VLLHHAADSEAQRRLV 495
Db 338 VIVLICHTWRLSGADQEKHDDSKINGILPVADLTTPPLRPKRWIVYADHPLYEVV 397
QY 496 GALAEALLRAALGGGRDVIWDLMEGRHVARVGPLMWAARTRVAREQGTVLLWLS---GA 552
Db 398 LKFAQLITAC--GTEVALDLLEEQVISEVGVMTVWSRQKQEMVESNKIILCSRGTA 455
QY 553 DLRPVSG-----PDPRAAPLALLHAAPR-----LALLAYFRLCAKGD 592
Db 456 KWKAILGWAEPVQLRCDHWKPAAGDLFTAAMNMILPDFKRPACFGTVVVCYFSGICSERD 515
QY 593 IPPPLRALPRYRL 606
Db 516 VPDLFNITSRYPLM 529

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Search completed: January 28, 2003, 09:31:17
Job time : 23 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run On: January 28, 2003, 09:30:38 : Search time 14 Seconds
(without alignments)
946.951 Million cell updates/sec

Title: US-09-863-818a-12
Perfect score: 3512
Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLECSRLREARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query % Match	Score	Length	ID	Description
1	2711	77.2	667	9	US-09-874-503-16
2	2711	77.2	667	9	US-10-000-157-16
3	2711	77.2	667	9	US-09-816-744-16
4	2711	77.2	667	9	US-09-747-259-16
5	1108	31.5	226	10	US-09-893-737-328
6	313	8.9	638	10	US-09-899-471-5
7	312.5	8.9	674	10	US-09-899-471-2
8	304.5	8.7	692	10	US-09-899-471-8
9	299	8.5	705	9	US-09-874-503-14
10	299	8.5	705	9	US-10-000-157-14
11	299	8.5	705	9	US-10-063-547-162
12	299	8.5	705	9	US-09-816-744-14
13	299	8.5	705	9	US-09-747-259-14
14	299	8.5	705	9	US-10-174-590-598
15	299	8.5	705	9	US-10-176-758-598
16	299	8.5	705	9	US-10-063-616-162
17	299	8.5	705	9	US-10-175-737-598
18	299	8.5	705	12	US-10-006-867-162
19	299	8.5	705	12	US-10-052-586-598

20	153	4.4	204	9	US-09-949-842-25	Sequence 25, Appl
21	123	3.5	810	10	US-09-809-567-3	Sequence 3, Appl
22	123	3.5	866	10	US-09-778-971-9	Sequence 9, Appl
23	123	3.5	866	12	US-10-033-522-1	Sequence 1, Appl
24	114.5	3.3	635	9	US-10-099-895-33	Sequence 33, Appl
25	113.5	3.2	2854	8	US-08-424-5508-394	Sequence 394, App
26	102	2.9	576	10	US-09-931-087A-1	Sequence 1, Appl
27	102	2.9	576	10	US-09-931-087A-21	Sequence 21, Appl
28	102	2.9	576	10	US-09-931-087A-22	Sequence 22, Appl
29	101	2.9	576	10	US-09-931-087A-23	Sequence 23, Appl
30	101	2.9	781	10	US-09-860-868-2	Sequence 2, Appl
31	101	2.9	994	10	US-09-852-909-2	Sequence 266, App
32	101	2.9	1089	9	US-10-174-590-266	Sequence 266, App
33	101	2.9	1089	9	US-10-176-758-266	Sequence 266, App
34	101	2.9	1089	9	US-10-175-737-266	Sequence 266, App
35	101	2.9	1089	12	US-10-052-586-266	Sequence 266, App
36	100	2.8	2862	10	US-09-743-659-5	Sequence 5, Appl
37	100	2.8	2864	10	US-09-743-659-2	Sequence 2, Appl
38	100	2.8	2865	10	US-09-742-659-6	Sequence 6, Appl
39	99.5	2.8	1168	9	US-09-935-868-24	Sequence 24, Appl
40	99	2.8	7257	9	US-10-014-717-5	Sequence 5, Appl
41	96.5	2.7	948	10	US-09-897-699-2	Sequence 7, Appl
42	95.5	2.7	954	9	US-09-944-413-7	Sequence 7, Appl
43	95.5	2.7	954	9	US-09-944-403-7	Sequence 7, Appl
44	95.5	2.7	954	9	US-09-944-896-7	Sequence 7, Appl
45	95.5	2.7	954	9	US-09-944-944-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1

US-09-874-503-16
; Sequence 16, Application US/09874503
; Patent No. US20020177188A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah G.
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa A.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vanden, Richard
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P3(US)
; CURRENT APPLICATION NUMBER: US/09/874,503
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/138,387

;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: US 60/134,287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US 60/131,022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: US 60/130,232
;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: US 60/113,621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/085,579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: US 09/854,208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: US 09/854,280
;; PRIOR FILING DATE: 2001-05-20
;; PRIOR APPLICATION NUMBER: US 09/816,744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: US 09/747,259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US 09/644,848
;; PRIOR FILING DATE: 2000-08-22
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;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: US 09/380,138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: US 09/311,832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: US PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: US PCT/US00/32678
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;; PRIOR FILING DATE: 2000-03-01
;; PRIOR APPLICATION NUMBER: US PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: US PCT/US99/31274
;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: US PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: US PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 16
;; LENGTH: 667
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-874-503-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
Best Local Similarity 77.5%; Pred. No. 1.1e-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

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QY 117 ---RGSCCLVVTCLRRATF-----PSPQOTS---PTRDFALKGNLRIQRHGKVFDP 163

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Db 145 ISHKGLRSKRTQSDPETWESLPRDSQRGGGPEFSFDLLPEARAIRVTITSSGPEVSRL 204
QY 214 CHOWALECEELSSPYDVQKIVSGGHTVELPYELLPCLCIEASYLOEDTVRRKKCPQSW 273
Db 205 CHOWALECEELSSPYDVQKIVSGGHTVELPYELLPCLCIEASYLOEDTVRRKKCPQSW 264
QY 274 PEAYGSDFWKSVHFTDYSHQTMVMALTLRCPLKLEALCORHWHHTLCKDLNATARES 333
Db 265 PEAYGSDFWKSVHFTDYSHQTMVMALTLRCPLKLEALCORHWHHTLCKDLNATARES 324
QY 334 DGWYVLEKVDLHPOLCFKVPWFSGNSSHVECPHQTSLSWNVSMDTQAQQLILHFS 393
Db 325 DGWYVLEKVDLHPOLCFK-----FSGNSSHVECPHQTSLSWNVSMDTQAQQLILHFS 380
QY 394 RMHATFSAAWSLPGLGQDTLVPVTVTSQ-----VWRSVQVF 430
Db 381 RMHATFSAAWSLPGLGQDTLVPVTVTSQARGSSPVSLDLIIPFLPGCCVLVNRSVQVF 440
QY 431 AWKHLCPDVSYRHLGLLILALLALLLLGVVLTALTCRRPQSGPGPARPVLLHHAADSEA 490
Db 441 AWKHLCPDVSYRHLGLLILALLALLLLGVVLTALTCRRPQSGPGPARPVLLHHAADSEA 500
QY 491 QRRVLGALAEILLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAAARTVARBOGTVLLWS 550
Db 501 QRRVLGALAEILLRAALGGGRDVIVDLWEGRHVARVGPLPWLWAAARTVARBOGTVLLWS 560
QY 551 GADLRVSGDPDRAAPLALLHAAAPRPLLLLAYFSLCAKGDIPPPRALPRYRLRLDLP 610
Db 561 GADLRVSGDPDRAAPLALLHAAAPRPLLLLAYFSLCAKGDIPPPRALPRYRLRLDLP 620
QY 611 RLLRALDARPPAEATSWGRLGARQRORQSRLCSRLEREAAARLADLG 657
Db 621 RLLRALDARPPAEATSWGRLGARQRORQSRLCSRLEREAAARLADLG 667

RESULT 2
US-10-000-157-16
; Sequence 16, Application US/10000157
; Publication No. US20020182673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J.Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P.Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1CIP4(US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21

;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/138387
;; PRIOR FILING DATE: 1999-06-09
;; PRIOR APPLICATION NUMBER: 60/172096
;; PRIOR FILING DATE: 1999-12-23
;; PRIOR APPLICATION NUMBER: 60/175481
;; PRIOR FILING DATE: 2000-01-11
;; PRIOR APPLICATION NUMBER: 60/191007
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/2113807
;; PRIOR FILING DATE: 2000-06-22
;; PRIOR APPLICATION NUMBER: 60/242837
;; PRIOR FILING DATE: 2000-10-24
;; PRIOR APPLICATION NUMBER: 60/244072
;; PRIOR FILING DATE: 2000-10-26
;; PRIOR APPLICATION NUMBER: 60/253646
;; PRIOR FILING DATE: 2000-11-28
;; PRIOR APPLICATION NUMBER: 09/311832
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 09/380138
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/380142
;; PRIOR FILING DATE: 1999-08-25
;; PRIOR APPLICATION NUMBER: 09/644848
;; PRIOR FILING DATE: 2000-08-22
;; PRIOR APPLICATION NUMBER: 09/747259
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: 09/816744
;; PRIOR FILING DATE: 2001-03-22
;; PRIOR APPLICATION NUMBER: 09/854208
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/854280
;; PRIOR FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: 09/874503
;; PRIOR FILING DATE: 2001-06-05
;; PRIOR APPLICATION NUMBER: 09/908827
;; PRIOR FILING DATE: 2001-07-18
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 09/929404
;; PRIOR FILING DATE: 2001-08-13
;; PRIOR APPLICATION NUMBER: 09/931836
;; PRIOR FILING DATE: 2001-08-16
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: 1999-03-08
;; PRIOR APPLICATION NUMBER: PCT/US99/10733
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: PCT/US99/31274
;; PRIOR FILING DATE: 1999-12-30
;; PRIOR APPLICATION NUMBER: PCT/US00/04341
;; PRIOR FILING DATE: 2000-02-18
;; PRIOR APPLICATION NUMBER: PCT/US00/05601
;; PRIOR FILING DATE: 2001-03-01
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: 2000-03-02
;; PRIOR APPLICATION NUMBER: PCT/US00/07532
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: PCT/US00/15264
;; PRIOR FILING DATE: 2000-06-02
;; PRIOR APPLICATION NUMBER: PCT/US00/23328
;; PRIOR FILING DATE: 2000-08-24
;; PRIOR APPLICATION NUMBER: PCT/US00/30873
;; PRIOR FILING DATE: 2000-11-10
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: PCT/US00/34956
;; PRIOR FILING DATE: 2000-12-20
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: PCT/US01/17800

;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/21066
;; PRIOR FILING DATE: 2001-06-29
;; PRIOR APPLICATION NUMBER: PCT/US01/21735
;; PRIOR FILING DATE: 2001-07-09
;; NUMBER OF SEQ ID NOS: 39
;; SEQ ID NO 16
;; LENGTH: 667
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-000-157-16

Query Match 77.2%; Score 2711; DB 9; Length 667;

Best Local Similarity 77.5%; Pred. No. 1.1e-215;

Matches 548; Conservative 15; Mismatches 54; Indels 90; Caps 11;

QY 1 MGSSRLAALLPLLLIIVIDLSDSAGIGFRLPLPHWNTCPILASHTEVLPISLAAPGGPSSP 60
DB 1 MGSSRLAALLPLLLIIVIDLSDSAGIGFRLPLPHWNTCPILASHTD----- 45
QY 61 QSLGVCSGTVPVAVCASICCOVAQVFNAGSSTSMCRNPKSLPHSSSIGDTRCQHLL---- 116
DB 46 -----DSFTGSSAVIPCTWML--FSTKPKW---VRWHCSR---CLCQHLLSGGS 89
QY 117 ---RGSCCLVVTCLRRRAITP-----PSPQTS---PTRDFALKGNLRIGRKVFPD 163
DB 90 GLQGLFHLVQKSKSTFKYRRHKMPAPQAKLLPRRHLSEKSHHISPS-----PD 144
QY 164 WTKGM:-----EVGTGYNRRWVQLSGGPEFSDLLPEARAIRVTISSGPEVSRL 213
DB 145 ISHGLRSKRTQSDPETWESLPRLDSQRHGGEFSDLLPEARAIRVTISSGPEVSRL 204
QY 214 CHOWALECEELSSPDYQKIVSGGHTVELPEYFELLPCLCIEASYLQEDTVRRKKCPQSW 273
DB 205 CHOWALECEELSSPDYQKIVSGGHTVELPEYFELLPCLCIEASYLQEDTVRRKKCPQSW 264
QY 274 PEAYGDFWKSVIHFTDYSQHTQVMALTLCPLKLEALCORHDWHTLCKDLNPATARES 333
DB 265 PEAYGDFWKSVIHFTDYSQHTQVMALTLCPLKLEALCORHDWHTLCKDLNPATARES 324
QY 334 DGWTVLEKVDLHPOLCFKVPWFSGNSHVCEPHQTSLSWNVSMDOCAQOLILHFSS 393
DB 325 DGWTVLEKVDLHPOLCFK----FSGNSHVCEPHQTSLSWNVSMDOCAQOLILHFSS 380
QY 394 RMHATFSAANSLPGLQDITLPPVYTVSQ-----VYRSDVQF 430
DB 381 RMHATFSAANSLPGLQDITLPPVYTVSQARSSPSVSLDLIIPFLRPGCCVLVWRSVQF 440
QY 431 AWKHLICPDVSYRHLGLLIIALLLTLGLVVALTCRRPQSGGPARPVLLLHAADSEA 490
DB 441 AWKHLICPDVSYRHLGLLIIALLLTLGLVVALTCRRPQSGGPARPVLLLHAADSEA 500
QY 491 QRLVGLALAEALLRAALGGGRDVIIVLWEGRHVARVGPLWLVAAARTVAREQCTVLLLWS 550
DB 501 QRLVGLALAEALLRAALGGGRDVIIVLWEGRHVARVGPLWLVAAARTVAREQCTVLLLWS 560
QY 551 GADLRVSGDPPRAAPLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 610
DB 561 GADLRVSGDPPRAAPLALLHAAPRLLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 620
QY 611 RLLRALDARFAEATSWRLGARQRQSRLELCSRLEREAAARLADLG 657
DB 621 RLLRALDARFAEATSWRLGARQRQSRLELCSRLEREAAARLADLG 667

RESULT 3

US-09-816-744-16

; Sequence 16, Application US/09816744

; Publication No. US20030003546A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P2(US)
; CURRENT APPLICATION NUMBER: US/09/816,744
; PRIOR FILING DATE: 2001-03-22
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-816-744-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
Best Local Similarity 77.5%; Pred. No. 1.le-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSSRLAALLPLLLIVDLSAGTGFPHLPHWNTROPCLASHTVLPISLAAPGGPSSP 60
DB 1 MGSSRLAALLPLLLIVDLSAGTGFPHLPHWNTROPCLASHTD----- 45
QY 61 QSLGVCESTVPVAVCASICCCQVAFNGASSTWCNRPKSLPHSSISGDTRCQHLL---- 116
DB 46 -----DSFTGSSAYIPCRTWAL--FSTRPWC---VRVWHCSR---CLCQHLLSGS 89
QY 117 ---RSGCCLVVTCLRAITF-----PSPQTS--PTRDFALGPNLRIGRHGKVPFD 163
DB 90 GLOGLFHLVLVOKSKSTFKFYRRHKMPAPQAQRKLLPRRHUSEKSHHISIPS-----PD 144
QY 164 WTHKGM-----EVGTGYNRRWVQLSGGPFESFDLLPEARAIKVTISSGPEVSRL 213
DB 145 ISHKLGRSKRTQSPDETWESEPLRDSQRHGPGPFESFDLLPEARAIKVTISSGPEVSRL 204
QY 214 CHOWALECEELSPDYVQKIVSGGHTVELPYEFLPCICIEASYLOEDTVRRKKCPFSQW 273
DB 205 CHOWALECEELSPDYVQKIVSGGHTVELPYEFLPCICIEASYLOEDTVRRKKCPFSQW 264
QY 274 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCQRHDWHTLCQLPNATARES 333
DB 265 PEAYGDFWKSVMHFTDYSOHTQVMWALTURCPKLEAALCQRHDWHTLCQLPNATARES 324
QY 334 DGWYVLEKVDLHPQLCFKVPWFSGNSHVECPHQGTSLTSWNSYMDTQAQQLILHFSS 393
DB 325 DGWYVLEKVDLHPQLCFK---FSGNSHVECPHQGTSLTSWNSYMDTQAQQLILHFSS 380
QY 394 RMHATSAWSLPGLCQDPLVPVTVTSQ-----VWRSDDVQF 430
DB 381 RMHATSAWSLPGLCQDPLVPVTVTSQ-----VWRSDDVQF 440
QY 431 AKWHLLCPDVSYSYHGLLILALILTLGVVLTALTCRRPQSGPGPARPVLLLHAADSEA 490
DB 441 AKWHLLCPDVSYSYHGLLILALILTLGVVLTALTCRRPQSGPGPARPVLLLHAADSEA 500
QY 491 QRLVGALAEELRAALGGGRDVTDLWEGRHVARVGPPLPWLNAARTVAREOGTVLLIWS 550
DB 501 QRLVGALAEELRAALGGGRDVTDLWEGRHVARVGPPLPWLNAARTVAREOGTVLLIWS 560
QY 551 GADLRVSGDPDPAAPLLALLHAAPRPLLLAYFSLCAKAGDIPPLRALPRYLLRLDLP 610
DB 561 GADLRVSGDPDPAAPLLALLHAAPRPLLLAYFSLCAKAGDIPPLRALPRYLLRLDLP 620
QY 611 RLLRALDARPFATSWGRLGARQRRQSRLELCSRLEREARLADLG 657
DB 621 RLLRALDARPFATSWGRLGARQRRQSRLELCSRLEREARLADLG 667

RESULT 4
US-09-747-259-16
; Sequence 16, Application US/09747259
; Publication No. US20030008815A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1(US)
; CURRENT APPLICATION NUMBER: US/09/747,259
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/213,087
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 16
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-747-259-16

Query Match 77.2%; Score 2711; DB 9; Length 667;
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Best Local Similarity 77.5%; Pred. No. 1.1e-215;
Matches 548; Conservative 15; Mismatches 54; Indels 90; Gaps 11;

QY 1 MGSSRLAALLPLLLIIVIDLSDSAGIGFRHLPHWNTCPPLASHTVPLPISLAAPGPPSSP 60
Db 1 MGSSRLAALLPLLLIIVIDLSDSAGIGFRHLPHWNTCPPLASHTD-----45

QY 61 QSLGVCBSGRVPAVCASICQVAFNGASSTWCNRNPKSLPHSSSIGDTRCOHLL---116
Db 46 -----DSFTGSSAIPCRTWWAL--FSTKFWC-----VRVWCSR--CLCOHLLSGGS 89

QY 117 ---RGSCCLVVTCLURRAITP-----PSPQTS---PTRDFALKGNLRIORHGKVFDP 163
Db 90 GLQGLPHLLVQKSKSSTFKFYRRHKMPAPAKRLPRRLHSEKSHHISIPS-----PD 144

QY 164 WTHKGM:-----EVGTGYNRWVQLSGPPEFSDLLPEARAIRVTISSGPEVSRL 213
Db 145 ISHGLRSKRTQSDPTWESLPRLSQRHGPEFSDLLPEARAIRVTISSGPEVSRL 204

QY 214 CHOWALECEELSSPDYDQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 273
Db 205 CHOWALECEELSSPDYDQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 264

QY 274 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCQRHDWHTLCKDLPNATARES 333
Db 265 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCQRHDWHTLCKDLPNATARES 324

QY 334 DGWYVLEKVDLHPQLCFKVPWFSEGNSSHVCEPHQTGSLTSWNVSMDTQAQOLILHFS 393
Db 325 DGWYVLEKVDLHPQLCFK-----FSGNSSHVCEPHQTGSLTSWNVSMDTQAQOLILHFS 380

QY 394 RHATFSAWSSLPGLGODTLVPPVYVSQ-----VWRSDVOF 430
Db 381 RHATFSAWSSLPGLGODTLVPPVYVSQARGSSPVSLDIIIPFLRPGCCVLRWRSOVQ 440

QY 431 AKWHLCPDVSYRHLGLIILALITLLGVVLAITCRRPQSGPGPARPVLLHAADSEA 490
Db 441 AKWHLCPDVSYRHLGLIILALITLLGVVLAITCRRPQSGPGPARPVLLHAADSEA 500

QY 491 QRLVLAELALLRAALGGGRDVTVDLWEGRHVARVGPPLWMAARTVAREOGTVLLLWS 550
Db 501 QRLVLAELALLRAALGGGRDVTVDLWEGRHVARVGPPLWMAARTVAREOGTVLLLWS 560

QY 551 GADLRVSGDPDRAAPLLALLHAAPRLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 610
Db 561 GADLRVSGDPDRAAPLLALLHAAPRLLLAYFSRLCAKGDIPPLRALPRYLLRLDLP 620

QY 611 RLRLALDARPPFAEATSWGLRGARQRQSRLELCSRLREARLADLG 657
Db 621 RLRLALDARPPFAEATSWGLRGARQRQSRLELCSRLREARLADLG 667

RESULT 5
US-09-893-737-328
; Sequence 328, Application US/09893737
; Patent No. US20020110855A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Presnell, Scott R.
; TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
; FILE REFERENCE: 00-41
; CURRENT APPLICATION NUMBER: US/09/893,737
; PRIOR FILING DATE: 2001-06-28
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 329
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 328
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-893-737-328

Query Match 31.5%; Score 1108; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 4.3e-84;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 VSYRHGLGLITALLALLTLLGVVLAITCRRPQSGPGPARPVLLHAADSEAQRRLVGALA 499
Db 9 VSYRHGLGLITALLALLTLLGVVLAITCRRPQSGPGPARPVLLHAADSEAQRRLVGALA 68

QY 500 ELLRAALGGGRDVTVDLWEGRHVARVGPPLWMAARTVAREOGTVLLLWSGADLRPVSG 559
Db 69 ELLRAALGGGRDVTVDLWEGRHVARVGPPLWMAARTVAREOGTVLLLWSGADLRPVSG 128

QY 560 PDPRAAPLLALLHAAPRLLLAYFSRLCAKGDIPPLRALPRYLLRLDLPRLRALDAR 619
Db 129 PDPRAAPLLALLHAAPRLLLAYFSRLCAKGDIPPLRALPRYLLRLDLPRLRALDAR 188

QY 620 PFAEATSWGLRGARQRQSRLELCSRLREARLADLG 657
Db 189 PFAEATSWGLRGARQRQSRLELCSRLREARLADLG 226

RESULT 6
US-09-899-471-5
; Sequence 5, Application US/09899471
; Patent No. US20020146763A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: Murine Cytokine Receptor
; FILE REFERENCE: 00-46
; CURRENT APPLICATION NUMBER: US/09/899,471
; CURRENT FILING DATE: 2001-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 698
; TYPE: PRT
; ORGANISM: mouse
US-09-899-471-5

Query Match 8.9%; Score 313; DB 10; Length 698;
Best Local Similarity 25.1%; Pred. No. 7.3e-18;
Matches 180; Conservative 77; Mismatches 291; Indels 168; Gaps 34;

QY 32 PHWNTCRPLASHTV-----LPTSL-AARGSPSSQSLGV-----CESGTVPAVCASI 78
Db 27 PDDTARCSLGLSCHLWDGDLVCLPGSLQSAPEGVLVPTRLQTELVLRCPQKT---DCA-- 81

QY 79 CCQVAVFNGASSTWCNRNPKSLPHSSSIGDTR-----CQHLRGSCCLVVTCLRRATF 133
Db 82 -LRVRVVVHLAVHGHWAPEEAGKSDSELQESRNASLQAQVVLFSQAYPIARCALLEVQV 140

QY 134 PS-----PPQTSPTDRF-----ALKGNLRIORHGK-----VFPDWTGHKMEVGTG 174
Db 141 PADLVQPGQSVGSVAFDCFEASLGAEOIWSYTKPRYQKELNLTAQLPDC--RGLEVRDS 198

QY 175 YNRWV-----OLSGGPEFSFDL-----LPEARIRVTISSGPEVSRL 213
Db 199 IQSCWVLPWLVSTGDGNNVLLTLDVSEEQDFSLYLRPVDA-----L 242

QY 214 CHOWALECEELSSPDYDQKIVSGGHTVELPYEFLLPCLCIEASYLQEDTVRRKKCPQSW 273
Db 243 KSLW-----YKNLTGPGQNTLNHTDLVPLCLIQVWLEPDSERVEFCPRD 289

QY 274 PEAYGDFWKSVMFTDYSQHTQVMVMAITLRCPLKLEAALCQRHDWHTLCKDLP-----PN 327
Db 290 PCAH--RNLLW---HIALRLVLSPGVMQLDAPCCLPGKVTLCWQADPQSPQPLVPVPQKN 345

QY 328 ATARESDGWYVLEKVDLHPQLCFKVPWFSEGNSSHVCEPHQTGSLTSWNVSMDT-QAQQ 386
Db 346 ATVNEPQDF---QLVAGHPNLCVQVSTW-----EKVOL-----OACSWADSLGPFKDDM 391

QY 387 LILHFSRRMHTAF-----SAAWSLPG-----LGQDTLVP--PVYTVSQVWRSD-VQF 430
Db 387 LILHFSRRMHTAF-----SAAWSLPG-----LGQDTLVP--PVYTVSQVWRSD-VQF 430

Db 392 LLVEMKTLGNTSVCALEPSCGCTPLPMSASTRAARLGEELLQDFRSHQCMQLWNNDDNMG 451
 QY 431 AKHLLCPDVSYRHG--LLIALLALLLLGWVLTALTCRRQSGPGPARPVLLLHADS 488
 Db 452 LW--ACPMKDYIHRWVWLVWCLLAAALFFLLKKDRKAARG-SRTALLLHSDG 507
 QY 489 EAQRRLVGALELLRAALGGGRDVIIVDLWEGRHVARVGLPWLWAARTVAREQGTVLIL 548
 Db 508 AGYERLVGALASALSOM--PLRVAVDLWSRRELSAHGALANFHQRRRLLOEGGVWILL 564
 QY 549 WSGA-----DLRPVS-GDPRAAPLLA-----LLHAAPRPLLLAYFRLCAKGI 593
 Db 565 FSPAQAQCOOVLQOTVEPGPHDALAAMLSCVLPDFLOGRATGRVGVYFDGLLHPDSV 624
 QY 594 PPLRALPRYRLRLDLPRLRLALDARPAEATSWGLGARQRR-----QSRLELCS 644
 Db 625 PSPFRVAPLFSLTQLPALFDALQG---GCSTSAGRPARVERVTOALRSALDSCT 677

RESULT 7

US-09-899-471-2
 ; Sequence 2, Application US/09899471
 ; Patent No. US20020146763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Murine Cytokine Receptor
 ; FILE REFERENCE: 00-46
 ; CURRENT APPLICATION NUMBER: US/09/899,471
 ; CURRENT FILING DATE: 2001-07-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 674
 ; TYPE: PRT
 ; ORGANISM: mouse
 US-09-899-471-2

Query Match 8.9%; Score 312.5; DB 10; Length 674;
 Best Local Similarity 25.3%; Pred. No. 7.7e-18;
 Matches 171; Conservative 65; Mismatches 276; Indels 165; Gaps 31;
 QY 96 RNP-KSLPHSSSIGDT-RQ-----HLRGSCCLVVTCLLRAITFPSPQSPTR---D 144
 Db 14 RNPVWSLERLMEPDQTARCSGLSCHLWDGD---VLCILPGSAPGFLVLPTRLQTE 69
 QY 145 FALKGP-----NLRQRHGKVFDPWT---HKGMEVGTGYNRRWVQLSGGPEFSDLPL 194
 Db 70 LVURCPQKTDCALRVRVVHVAHGHWAEPPEAGKSDSELSQESRNASLQAQVVLSEQATP 129
 QY 195 EARAIRVTI-----SSGPEVSRYLCHOWA-----WSYTKPRYQKELNLT 184
 Db 130 IARCALLEVQVPADLVQPGQSVGSVAFDCFEASLGAEVQI-----WSYTKPRYQKELNLT 184
 QY 219 -----LECEELSPYDVQ-----KIVSGGHTVELPYEFLLPCLC 252
 Db 185 QQLPDGDNVLITLDVSEQDFSELLYLRVPDALKSLWKNTITLHNDLVPCLC 244
 QY 253 IEASYLQEDTVRRKCPQFQSWPAGSDFWKSVHFTDYSQHTOMVALTLRCPKLVEAAL 312
 Db 245 IQWLSPEPDSERVEFCFPREDPGAH-RNLW---HIARLVLSGVWQLDAPCCLPKKVTL 300
 QY 313 QRHDHHTLCKDL-----PNATARES DGWVLEKVDLHPQLCFKVPWFSGNSSHVEFC 366
 Db 301 CWQAPDQSPQPLVPVPVPOKRNATVNEPDF---QLVAGHPNLCVQVSTW-----EKVQL 351
 QY 367 PHQTGSLTSNWSMDT-QAQQILHLSRMRHATF-----SAAWSLPG-----LGQD 411
 Db 352 -----QACSWADSLGPPKDDMLLVMKMTGLNNTSVCALEPSCGCTPLPMSASTRAARLGE 406
 QY 412 TLVP-PVYTVSQWRSD-VQFAKHLCLCPDVSYRHG--LLIALLALLITLLGWLTALTC 467
 Db 407 LLQDFRSHQCMQLWNNDDNMGSLW---ACPMKDYIHRWVWLVWCLLAAALFFLLKK 463

QY 468 RRQSGPGPARPVLLLHAADSEARQLVGLAELLRAALGGGRDVIIVDLWEGRHVARVGP 527
 Db 464 DRKAARG-SRTALLLHSDAGYERLVGALASALSOM--PLRVAVDLWSRRELSAHGA 519
 QY 528 LPWLWAARTVAREQGTVLLWSGA-----DLRPVS-GDPRAAPLLA-----LLH 572
 Db 520 LAWFHHQRRRLQEGGVVILLFSPAQAQCOOVLQOTVEPGPHDALAAMLSCVLPDFLQ 579
 QY 573 AAPRPLLLAYFRLCAKGI DPPPLRALPRYRLRLDLPRLRLALDARPAEATSWGLGA 632
 Db 580 GRATGRYGVVFDGLLHPDSVSPFRVAPLFSLTQLPALFDALQG---GCSTSAGRPA 636
 QY 633 RQRR-----QSRLELCS 644
 Db 637 RVERVTOALRSALDSCT 653

RESULT 8

US-09-899-471-8
 ; Sequence 8, Application US/09899471
 ; Patent No. US20020146763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: Murine Cytokine Receptor
 ; FILE REFERENCE: 00-46
 ; CURRENT APPLICATION NUMBER: US/09/899,471
 ; CURRENT FILING DATE: 2001-07-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 692
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-899-471-8

Query Match 8.7%; Score 304.5; DB 10; Length 692;
 Best Local Similarity 25.4%; Pred. No. 3.6e-17;
 Matches 176; Conservative 69; Mismatches 246; Indels 203; Gaps 36;
 QY 36 TRCPILASHTVELPISLAAPGPPSSPSQL---GVCESGTVPAVCASICCCQVAQVFNAGASS 91
 Db 78 TDCDLCLR---VAVILAVHGWEEPEDEEKFGGAADSGVEEPNALSQAQVVLSEFQ 133
 QY 92 TSWC-----RNPKSL-PHSSSIGDTRCQHLRGSCCLVVTCLLRAITFPSPQSPTRDF 145
 Db 134 TARCVLLEVVQVPAALVQFGQSVGS-----VYDCFEAAL-----GSEVRW 174
 QY 146 ALKGNLRLIQ-RHGKVFV-----DWTGKMEVGT-----GYNRRWVQLSGGPEFS 189
 Db 175 SYTPRYEKELNHTQOLPALPWLNVSDGDNVHLVNLVSEQHFGSLYWNQVQGPVK-- 232
 QY 190 FDLLEPRAIRVTISSGPEVSRYLCHOWALECELSSPYDQKIVSGGHTVELPYEFLLP 249
 Db 233 -----PRW-----HKNLGTGQIITLHNTDLVP 254
 QY 250 CUCIEASYLQEDTVRRKCPQFQSWPAGSDFWKSVHFTDYSQHTOMVALTLR----- 303
 Db 255 CLCICQWPLEPDSVRTNICPFREDPRAH-QNLWQAAR-----LRLTLQSLWLLDA 303
 QY 304 CPLKLEALCORHDHHTLCKDL-----PNATARES DGWVLEKVDL--HPOLCFKVP 354
 Db 304 PCSLPAEALCWRAPGGDCQPLVPLSWENVTVDK-----VLEPPLKHPNLCVQV-- 356
 QY 355 WFSFGNSSH---VBC---PHQTGSLTSNWSMDTQAQQILHLSRMRHATF--SAAWSL 406
 Db 357 -----NSSEKLOLQCEWLADSLGPLKDDVLLLETRGPQ-----DNRSLEPSCSCTSLP 406
 QY 407 G-----LGQDTPVPVYTVS-----QVWRSDVQFAKHLCLCPDVSYRH--LGILL 448
 Db 407 SKASTRAARLGE-----YLLQDLQSGCQLQWLWDDDLGALW---ACPMKDYIHRWV 456
 QY 449 IIALALLITLLGWLTALTCRRPQSGPGPARPVLLLHAADSEARQLVGLAEL-----LR 503

Db 457 WLACLLFAAALSLLLLK-KDHAKAAARGRAALLLYSADDSGFERLVGALASALCOLPLR 515
Qy 504 AALGGGRDVTDLWEGRHVARVGLPWLMAARTVRAREOCTVLLLSGADLR----- 555
Db 516 VA-----VLSRRELSAQGPVAFHQAQRQTLOEGGVVLLSPGAVALLCSEWLQD 567
Qy 556 PVSGP---DRAAPLALLHAAPRL-----LLLAYFSRLCAKGDIPPLRALPRYL 605
Db 568 GVSQPGAHGPHDAFRASLSVLPDFLQGRAPGSYVGCDFRLLHPDAVPALFRTVPVFTL 627
Qy 606 LRDLPRLLRALDARPPFAEATSWRLGARQRQR 639
Db 628 PSQLPDFLQALQ-QPRAPRS--GRLOBRAEQVSR 658

RESULT 9
US-09-874-503-14
; Sequence 14, Application US/09874503
; Patent No. US2002017186A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah G.
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasnik, Melissa A.
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381C1P3(US)
; CURRENT APPLICATION NUMBER: US/09/874,503
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/253,646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: US 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: US 60/134,287
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: US 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: US 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-20
; PRIOR APPLICATION NUMBER: US 09/816,744

; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: US PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: US PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: US PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: US PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: US PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-874-503-14

Query Match 8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.1e-16;
Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

Qy 36 TRCPILASHTEVLPISLAAGPGSPQSL-----GYCESGTVPACVASICCCQVAVENGASS 91
Db 78 TDCDLCLR---VAVHLAVHGHWEPEDEKEKFGGAADSGVEEPNRSQAQVVLSEFQ-AYP 133
Qy 92 TSWC-----RNPXSL-PHSSSIGTRCOHLRLGSCCLVVTCLRRITFPSPQTSPTDRF 145
Db 134 TARCVLLEVQVPAALVQFGQSVGS-----VVYDCFEAAL-----GSEVRW 174
Qy 146 ALKGNLRIQ-RHGKVP-----DWTGKMEVGT-----GYNRWVQLSGGPEFS 189
Db 175 SYTPRYEKELNHTQQLPALPWLNVNVSADGNVHLVNLVNSERQHFGLSLYNQVQGPVK-- 232
Qy 190 FDLLEPEARIRVTISSGPEVSRVLRCHOWALECEELSPYDVQKIVSGGHTVVELPYELLP 249
Db 233 -----PRW-----HKNLTPQITLNLHTOLVP 254
Qy 250 CLCTEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYSOHTOMVMALTLR----- 303
Db 255 CLCIQVWPLEPDSVRTNICPREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
Qy 304 -CPLKLEAALCQRDWHITLCKDL-----PNATARESDGWVLEKVDL---HPQLCFKVP 354
Db 304 PCSLPFAEAALCWRAPGGDPCCQPLVPPLSWENVTYDK-----VLEFPLKGNLVCQV-- 356
Qy 355 WFSFGNSSH-----VEC--PHQTGSLTSNWNVSMDTQAQQLILHFSRMRHATF--SAASL 406

Db 357 -----NSSEKQLQECWADSLGPKDDVLLLETRGPQ-----DNRSLCALEPSPGCTSLP 406
QY 407 G-----LQDTLPVPYTVTS-----QWRSDDVQFANKHLLCPDVSYEH-----444
Db 407 SKASTRAARLE-----YLLQDLOSQCQLWDDDLGALW---ACPMDKYIHKRWALV 456
QY 445 --LGLLLALALLTLGV-----VLALTCRRPQSGPGP--ARPVLLHHAADSEAQRRLVG 496
Db 457 WLACLLFAAALSILLKKDHKANGWLRLKQDVRSGAAARGRAALLLYSADPSGFERLVG 516
QY 497 ALABEL-----LRAALGGRRDVIYDLWEGRHVARVGPLWMLWAARTVAREQGTVLLWVG 551
Db 517 ALASALCOLPRVA-----VDLWSRRELSAQGPVAFHQAORRQTLQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DPPRAAPLLALLHAAPRL-----LLLAYFSLCAKGD 593
Db 569 GAVALCSEWQDGVSGFGANGPHDAFRASLSVLPDLOGRPGSVYGACFDRLHHPDAV 628
QY 594 PPPLRALPRVRLRLDLPRLRALDARPFABEATSWGRIGARQRQR 639
Db 629 PALFRTVPVTLPSQLPDFLQALQ-QPRAPRS---GRLOERAEQVSR 671

RESULT 10

US-10-000-157-14
; Sequence 14, Application US/10000157
; Publication No. US20020192673A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul L.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Hymowitz, Sarah
; APPLICANT: Tumas, Daniel
; APPLICANT: Starovasinik, Melissa.
; APPLICANT: Vanlookeren, Menno
; APPLICANT: Vandien, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P4(US)
; CURRENT APPLICATION NUMBER: US/10/000,157
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242837
; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: 60/244072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/253646
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/908827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/931836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 14
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-000-157-14

Query Match 8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.1e-16;

Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

QY 36 TRCPPLASHTVLPISLAAGPSPSSQL-----GVCESGTVPVAVCASICQVAVFNGASS 91
Db 78 TDCDLCLR---VAVHLAVHGWEEPEDEKFGGAADSGVEEPRNASLQAVVLSFQ--AYP 133
QY 92 TSWC-----RNPKSL-PHSSSIGDTRCQHLRLGSCCLVVTCLRRATTFSPPTSPTRDF 145
Db 134 TARCVLLEQVPAALVQFGSVGS-----VYDCEFAAL-----GSEVRW 174
QY 146 ALKGNLRQ--RHGKVFPP-----DWHKGMVEGT-----GYNRRWVQLSGGPEFS 189
Db 175 SYTPRYEKELNHTQQLPALPMLNVSADGDNVHLVNVSEQHFGLSLYWVQVGPVK-- 232
QY 190 FDLLEPEARAIRVTISSGPEVSVRLCHQWALECEELSPDYQKIVSGGHTVELPEFLP 249
Db 233 -----PRW-----HKNLTGPQIITLNTHTDLP 254
QY 250 CLCIEASYLQEDTVRRKKCPFGSWPEAYGSDFWKSVHFTDYSHQTMVMALTLR----- 303
Db 255 CLCIQWPLEPDSVRTNICPFREDPRAH-QNLWQAAAR-----LRLTLQSWLLDA 303
QY 304 -CPKLEAALCORHDWHTLCKDL-----PNATARESDGWVYVLEKVDL--HPQLCFKVP 354
Db 304 PCSLPAEAALCWRAPEGDPQPLVPPPLSWENVTVDK-----VLEFPLKGGHNPCLVQV-- 356
QY 355 WFSFGNSH-----VEC--PHQTSLSWNVSMDTQAQOLILHFSRHMATF--SAAWSLP 406
Db 357 -----NSSEKLQOECLWADSLGPKDDVLLLETRGPQ-----DNRSCLALEPSGCTSLP 406
QY 407 G-----LGQDTLVPPVTVS-----QVWRSVQVFAKHLICPDVSYRH----- 444
Db 407 SKASTRAARLGE-----YLLQDLQSGOCQLQWDDDLGALW---ACPMKDIHKRWALV 456
QY 445 --LGLLILALLLTLTG-----VLALTCRRPQSGPGP-ARPVLLHHAADSEARRLVG 496
Db 457 WLACLLFAAALSILLKKHAKGWLRLKQDVSRAAGRAALLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIWLEGRHVARVGPPLWMAARTVAREOGTVLLWSG 551
Db 517 ALASALCOLPLRVA-----VWLWSRRELSAQGPVAFHQAQRQTQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DRAAPLALLHAAAPRL-----LILAYFSRLCAKGI 593
Db 569 GAVALCSEWLQGVSGPGAHPDAFRASLSVLPDFLQGRAPGSYVGACFDRLHHPDAV 628
QY 594 PPPLRALPRYLLRDLPRLLRALDARPPFAEATSWGRLGARQRQR 639
Db 629 PALFRTVPVFTLPSQLPDFLGALQ-QPRAPRS--GRLOERAEQVSR 671

RESULT 11
US-10-063-547-162
; Sequence 162, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,547
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 162

; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-547-162

Query Match 8.5%; Score 299; DB 9; Length 705;
Best Local Similarity 25.5%; Pred. No. 1.1e-16;
Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;

QY 36 TRCPPLASHTVLPISLAAGPSPSSQL-----GVCESGTVPVAVCASICQVAVFNGASS 91
Db 78 TDCDLCLR---VAVHLAVHGWEEPEDEKFGGAADSGVEEPRNASLQAVVLSFQ--AYP 133
QY 92 TSWC-----RNPKSL-PHSSSIGDTRCQHLRLGSCCLVVTCLRRATTFSPPTSPTRDF 145
Db 134 TARCVLLEQVPAALVQFGSVGS-----VYDCEFAAL-----GSEVRW 174
QY 146 ALKGNLRQ--RHGKVFPP-----DWHKGMVEGT-----GYNRRWVQLSGGPEFS 189
Db 175 SYTPRYEKELNHTQQLPALPMLNVSADGDNVHLVNVSEQHFGLSLYWVQVGPVK-- 232
QY 190 FDLLEPEARAIRVTISSGPEVSVRLCHQWALECEELSPDYQKIVSGGHTVELPEFLP 249
Db 233 -----PRW-----HKNLTGPQIITLNTHTDLP 254
QY 250 CLCIEASYLQEDTVRRKKCPFGSWPEAYGSDFWKSVHFTDYSHQTMVMALTLR----- 303
Db 255 CLCIQWPLEPDSVRTNICPFREDPRAH-QNLWQAAAR-----LRLTLQSWLLDA 303
QY 304 -CPKLEAALCORHDWHTLCKDL-----PNATARESDGWVYVLEKVDL--HPQLCFKVP 354
Db 304 PCSLPAEAALCWRAPEGDPQPLVPPPLSWENVTVDK-----VLEFPLKGGHNPCLVQV-- 356
QY 355 WFSFGNSH-----VEC--PHQTSLSWNVSMDTQAQOLILHFSRHMATF--SAAWSLP 406
Db 357 -----NSSEKLQOECLWADSLGPKDDVLLLETRGPQ-----DNRSCLALEPSGCTSLP 406
QY 407 G-----LGQDTLVPPVTVS-----QVWRSVQVFAKHLICPDVSYRH----- 444
Db 407 SKASTRAARLGE-----YLLQDLQSGOCQLQWDDDLGALW---ACPMKDIHKRWALV 456
QY 445 --LGLLILALLLTLTG-----VLALTCRRPQSGPGP-ARPVLLHHAADSEARRLVG 496
Db 457 WLACLLFAAALSILLKKHAKGWLRLKQDVSRAAGRAALLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIWLEGRHVARVGPPLWMAARTVAREOGTVLLWSG 551
Db 517 ALASALCOLPLRVA-----VWLWSRRELSAQGPVAFHQAQRQTQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DRAAPLALLHAAAPRL-----LILAYFSRLCAKGI 593
Db 569 GAVALCSEWLQGVSGPGAHPDAFRASLSVLPDFLQGRAPGSYVGACFDRLHHPDAV 628
QY 594 PPPLRALPRYLLRDLPRLLRALDARPPFAEATSWGRLGARQRQR 639
Db 629 PALFRTVPVFTLPSQLPDFLGALQ-QPRAPRS--GRLOERAEQVSR 671

RESULT 12
US-09-816-744-14
; Sequence 14, Application US/09816744
; Publication No. US20030003546A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel

Db 134 TARCVLLEQVPAALVQFGSGVS-----VYDCFEAAL-----GSEVRW 174
QY 146 ALKGNLRIO-RHGKVP-----DWTGKMEVGT-----GYNRRVQLSGGPEFS 189
Db 175 SYTOPRYEKLHNTQQLPALPWLNVADGNDVHLVNLVSEEQHFGSLYWNQVQPPK-- 232
QY 190 FDLLEPAAIRVTISSGPEVSRCHQWALECEELSSPYDVQKIVSGGHTVPELFFLP 249
Db 233 -----PRW-----HKNLGPGQIITLHNTDLP 254
QY 250 CLCIEASYLOEDTVRRKKCFQSWPEAYGDFWKSVMHTDYSHQTMWMLTLR----- 303
Db 255 CLCQVWPLEPDSVTRNICPEREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
QY 304 -CPLKEAALCORHDWHTLCKDL-----PNATARESDGWVYLEKVDL--HPQLCFKVP 354
Db 304 PCSLPAEALCWAPGGDCQPLVPLSWENVTVDK-----VLEPPLKGHPNLCVQV-- 356
QY 355 WFSFGNSH-----VEC--PHOTGSLTSMNVSMDTQAQQLILHFSRHMATF--SAAWSLP 406
Db 357 -----NSSEKLQLECLWADSLGPKDDVLLLETRGPQ-----DNRSICALPEPSGCTSLP 406
QY 407 G-----LGQDTLVPVTVS-----QWRSDVQFAWKHLLCPDVSYRH----- 444
Db 407 SKASTRAARLGE-----YLLQDLQSGQCQLQMDLGLALW---ACPMKDYIHKRWALV 456
QY 445 --LGLLILALLLTLLGV-----VLATCRRRQSGPGP-ARPVLLHHAADSEAOORLVG 496
Db 457 WLACLLFAAALSLLLLKKHAKGWLRLKQDVRSGAARGRAALLLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIWLEGRHVARVGPLWMLMAARTVAREOGTVLLWSG 551
Db 517 ALASALCOLPLRVA-----VDLWSRRELSAQGPVAFWFAHQRRQTLQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DPRAAPLALLHAAPRL-----LLLAYFSRLCAKADI 593
Db 569 GAVALCSEWLQDVGSGPGAHGPHDAFRASLVCVLPDLQGRAPGSYVGCDFRLLHPDAV 628
QY 594 PPLRALPRYLRLDRLPRLRLALDARPAEATSWGRLGARQRORSR 639
Db 629 PALFRTVPVFTLPSQLPDFLGLAQ-QPRAPRS--GRLOERAEOQVSR 671

RESULT 14
US-10-174-590-598
; Sequence 598, Application US/10174590
; Publication No. US20030008352A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C42
; CURRENT APPLICATION NUMBER: US/10/174,590
; CURRENT FILING DATE: 2002-06-18
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 598
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-590-598

Query Match

8.5%; Score 299; DB 9; Length 705;

Best Local Similarity 25.5%; Pred. No. 1.1e-16;
Matches 180; Conservative 69; Mismatches 243; Indels 214; Gaps 37;
QY 36 TRCPPLASHTVLPISLAAPGGPSSQSL-----GVCESGTVPACASICCCQVAQVNGASS 91
Db 78 TDCDLCLR---VAVHLAVGHWEPEDEEKFGGAADSVSEEPNRSALQAQVLSFQ-AYP 133
QY 92 TSWC-----RNPKSL-PHSSSIGDTRCOHLLRGSCCLVTRRAITFPSPQTSPTPRDF 145
Db 134 TARCVLLEQVPAALVQFGSGVS-----VYDCFEAAL-----GSEVRW 174
QY 146 ALKGNLRIO-RHGKVP-----DWTGKMEVGT-----GYNRRVQLSGGPEFS 189
Db 175 SYTOPRYEKLHNTQQLPALPWLNVADGNDVHLVNLVSEEQHFGSLYWNQVQPPK-- 232
QY 190 FDLLEPAAIRVTISSGPEVSRCHQWALECEELSSPYDVQKIVSGGHTVPELFFLP 249
Db 233 -----PRW-----HKNLGPGQIITLHNTDLP 254
QY 250 CLCIEASYLOEDTVRRKKCFQSWPEAYGDFWKSVMHTDYSHQTMWMLTLR----- 303
Db 255 CLCQVWPLEPDSVTRNICPEREDPRAH-QNLWQAAR-----LRLTLQSWLLDA 303
QY 304 -CPLKEAALCORHDWHTLCKDL-----PNATARESDGWVYLEKVDL--HPQLCFKVP 354
Db 304 PCSLPAEALCWAPGGDCQPLVPLSWENVTVDK-----VLEPPLKGHPNLCVQV-- 356
QY 355 WFSFGNSH-----VEC--PHOTGSLTSMNVSMDTQAQQLILHFSRHMATF--SAAWSLP 406
Db 357 -----NSSEKLQLECLWADSLGPKDDVLLLETRGPQ-----DNRSICALPEPSGCTSLP 406
QY 407 G-----LGQDTLVPVTVS-----QWRSDVQFAWKHLLCPDVSYRH----- 444
Db 407 SKASTRAARLGE-----YLLQDLQSGQCQLQMDLGLALW---ACPMKDYIHKRWALV 456
QY 445 --LGLLILALLLTLLGV-----VLATCRRRQSGPGP-ARPVLLHHAADSEAOORLVG 496
Db 457 WLACLLFAAALSLLLLKKHAKGWLRLKQDVRSGAARGRAALLLYSADDSGFERLVG 516
QY 497 ALAEL-----LRAALGGGRDVIWLEGRHVARVGPLWMLMAARTVAREOGTVLLWSG 551
Db 517 ALASALCOLPLRVA-----VDLWSRRELSAQGPVAFWFAHQRRQTLQEGGVVLLFSP 568
QY 552 ADLR-----PVSGP---DPRAAPLALLHAAPRL-----LLLAYFSRLCAKADI 593
Db 569 GAVALCSEWLQDVGSGPGAHGPHDAFRASLVCVLPDLQGRAPGSYVGCDFRLLHPDAV 628
QY 594 PPLRALPRYLRLDRLPRLRLALDARPAEATSWGRLGARQRORSR 639
Db 629 PALFRTVPVFTLPSQLPDFLGLAQ-QPRAPRS--GRLOERAEOQVSR 671

RESULT 15
US-10-176-758-598
; Sequence 598, Application US/10176758
; Publication No. US20030008353A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C104
; CURRENT APPLICATION NUMBER: US/10/176,758
; CURRENT FILING DATE: 2002-06-21

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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:28:18 ; Search time 22 Seconds
(without alignments)
2870.923 Million cell updates/sec

Title: US-09-863-818A-12
 Perfect score: 3512
 Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLECSRLEAREARLADLG 657

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database : PIR_73:**
1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	122	3.5	738	2	I49295	IL-12 receptor bet	
2	114.5	3.3	635	2	A45286	MPL-p protein prec	
3	113.5	3.2	923	2	A39596	progesterone recep	
4	111.5	3.2	515	2	G75267	ABC transporter, p	
5	110.5	3.1	381	2	S48049	cholecystokinin B	
6	107.5	3.1	452	2	A46195	cholecystokinin B	
7	105.5	3.0	923	2	I53280	progesterone recep	
8	105.5	3.0	7576	2	T17438	FK506 polyketide s	
9	105	3.0	523	2	A83106	hypothetical prote	
10	104	3.0	709	2	F75584	hypothetical prote	
11	104	3.0	732	1	JU0132	acylaminoacyl-pept	
12	103.5	2.9	401	2	T36882	hypothetical prote	
13	102.5	2.9	1034	2	JC5598	mucin - rat	
14	102	2.9	579	2	B45266	MPL-K protein prec	
15	102	2.9	829	2	B96640	hypothetical prote	
16	102	2.9	930	2	A25923	progesterone recep	
17	102	2.9	2035	2	AC0233	yersiniabactin bio	
18	102	2.9	2041	2	T17439	peptide synthetase	
19	101	2.9	428	2	S70670	3-deoxy-D-manno-2-	
20	101	2.9	482	2	GB3490	probable outer mem	
21	101	2.9	906	2	G83156	probable transcrip	
22	100.5	2.9	392	2	T46418	hypothetical prote	
23	100.5	2.9	1438	2	T17402	dihydroaeruginoinc	
24	100	2.8	1193	2	T50729	magnesium-protopor	
25	99	2.8	404	2	T35421	probable regulator	
26	99	2.8	560	2	T36054	probable two-compo	
27	98.5	2.8	756	2	F70815	hypothetical prote	
28	98	2.8	732	1	S07624	acylaminoacyl-pept	
29	97.5	2.8	452	2	JC2459	gastrin/cholecysto	

ALIGNMENTS

RESULT 1
I49295
IL-12 receptor beta component precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49295
J:Chua, A.O.; Chizzonite, R.; Desai, B.B.; Truitt, T.P.; Nunes, P.; Minetti
J. Immunol. 153, 128-136, 1994
A:Title: Expression cloning of a human IL-12 receptor component. A new member
A:Reference number: I37892; MUID:94267217; PMID:7911493
A:Accession: I49295
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-738 <RES>
A:Cross-references: EMBL:U23922; NID:q1046233; PIDN:AAA87457_1; PID:q1046233

Query Match 3.5%; Score 122; DB 2; Length 738;
Best Local Similarity 20.3%; Pred. NO. 0.3;
Matches 128; Conservative 61; Mismatches 183; Indels 260; Gaps 36;

QY	38	CPIASHTVLP	-----SLAAPGGSSPQSLGVCESGTVPAVCASICQVAVFGNASS	91
Db	218	CPSNMAQETIQ	RRRRRLSSGAPGGWSQWMPVC	254
QY	92	TSWCRNPKSUPHSS	IGDTRCOHLHSGCCLVVTCTLRRAITF--PSPQTSPTDRFALKG	149
Db	255	-----PEVLPOAKI	--KFLVEPLNOGG-----RRRLTMOGQSPQALNPE--GCRG	295
QY	150	-PNLRIQHGKVF	-----PDWTHKGMVEGTCYNNRWQLSGGPFSDLLPEARAIW	201
Db	296	RPAQYKKHLVLVRML	SCRCAQTSKTVPLGKKLN-----LSGA-TYDLNLVLAKTFRGSR	349
QY	202	TISSGPEVSRLCHOWALE	CEELSSPYDVQKIVYSGGHTVELPEYFLLP--CLCIEASYLQ	259
Db	350	TI-----QKWHLP	PAQELTETRLNVSV-GGNWTSQWMAQAQPTCYCLE-----	392
QY	260	EDTVRRKKCFQSQWPEAYG	SDFKWSYHFTDYSOHTQVMVALTRCLPKLEALCORHDWH	319
Db	393	-----WQPW-----	WQPNH-----FOHRNHT-----CTLVPEEDPAKMWTHSKS	424
QY	320	TLCKDLPNATAREDSQWYV--	LEKVDLHPOLCFKQPNWFSGNSS-----HVECPIHQ	369
Db	425	S-----KPTLEGE	ECYRITVFRASKNPKNPLMWATVLSYFEGGNASRAGTRPHVSRNQ	478
QY	370	TGSLTS--WNVSMDTQAQO	LIILHFSSRMHATFSAANSLPGLGQDTLVPVYTVSQV-----	423
Db	479	TGDSVSVENTASQLSCPG	VLQTYVYVRCAE--DGANE-----SEWLVP--FKTQVTLDG	530
QY	424	WRSQVOF-----	-----ANKHLLCP-----DVSYRHLGLLIAL-----LALLTLIG	460
Db	531	LKRSVMYKQVQRADTRAL	PELGAMSH---PORFSFEQVQISRLTSIFASLGFSFASVLVLSG	587

```
QY 461 VV-----LALTC----- 467
Db 598 YIGLNRAWHLCPLPTPGSTAVEFFPSQKQAWQCNPEDEFEVLYPRDALVEMPGD 647
QY 468 -----RRPQSGFGPA-----RVLILLHAADSEAQR-RLVGALAEILRAA----- 505
Db 648 RGDGTESPAAPCAEDTRRLP-----ETQRQVQALSEARRLGLAREDCPRGDLA 699
QY 506 -----LGG---GRDVTVDLWEGRHVARVGP 527
Db 700 HVTLPILLGGVTQAGASVLDLWRTHKTAEPGP 731

RESULT 2
A45266
MPL-P protein precursor - human
C:Species: Homo sapiens (man)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C:Accession: A45266
R:Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.
Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992
A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl
A:Reference number: A45266; MUID:92302297; PMID:1608974
A:Accession: A45266
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-635 <VIG>
A:Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
C:Keywords: transmembrane protein

Query Match 3.3%; Score 114.5; DB 2; Length 635;
Best Local Similarity 19.4%; Pred. No. 0.94;
Matches 111; Conservative 52; Mismatches 129; Indels 281; Gaps 34;

QY 31 LPHWNR-CPLASHTEV---LPI----- 52
Db 84 MPHFTRYCYQPPDQEEVRLFFPLHLWKNVFLNTRQTVLFDVDSGLPAPPSTIRKAMG 143
QY 65 VCESGTVPVAVCASICQVAQVFNAGSSTSW----- 106
Db 144 ----GSQP-----GELQISWEEPAPEISDELRYELRYGPRDPK----- 179
QY 107 IGTRCQHLLRGSCCLV-----TCLRRATTF-PSPQTSPTRD---FALKGP 150
Db 180 TGPVTIQLIATETCPALQRPHASALDQSPCAQPTMPQDGPQKQTSREASALTAEQG 239
QY 151 NLRIQRHGKGVFDPWTHKMGVEGTGYNRRWVQLSGGPEFSDLLPEARAIRVTISGGPEVS 210
Db 240 SCLI-----SGLPQNSY---WLQLRSEPD-----GISLGGSWG 270
QY 211 VRLCHQWALECELSPYDVQKIVSGGHTVELPYE-----FLLPCLCIEASYLQEDT 262
Db 271 ----SWSLPV-----TVDLPGDAVALGLQCTFLDLKNVTCWQQQDHD 308
QY 263 V-----RRKKCPFSQSP----- 274
Db 309 ASSQGFYHSRARCPCPRDRYPINWCEBEETNPGLQTPQFSRCHFKSRNDSIIHILVEV 368
QY 275 -----EAY-GSDEF-----KSHFTDYQSHTQWVMALTLRCLKLEAALCQRHD 317
Db 369 TPAPGTVSHYLGSPFIHQAVRLPPTNHLNREISSG-----HLELWQHPS 415
QY 318 W---HTLCKDLPNATARESOGWVYLE-----KYDLHPQLCFKVQ-----PW 355
Db 416 WAAQETCYQL-RYTGEGHQDWKLVLEPPLGARGGTLELRPSRYRLQLRARLNGPTYQGPW 474
QY 356 FSEGNSSHVECHPQGTGSLTSWNVSMDTQAOQLIL-----HFSRMRHAT 398
Db 475 SWSDDPRVE-----TATETAW-ISLVT-ALHLVLGLSAVLGILLRLRWQFPAYHRLRH-- 526
QY 399 FSAAW-SLPG-----LQO-----DT--LVPPVYTVS 421
Db 527 --ALWPSLDLHRVLGQYLDRDTAALSPPKATVS 557
```

RESULT 3

A39596

progesterone receptor B form - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 20-Aug-1999

C:Accession: A39596; I49111

R:Schott, D.R.; Shyamala, G.; Schneider, W.; Parry, G.

Biochemistry 30, 7014-7020, 1991

A:Title: Molecular cloning, sequence analyses, and expression of complementary DNA en

A:Reference number: A39596; MUID:91299759; PMID:2069958

A:Accession: A39596

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-923 <SCH>

A:Cross-references: GB:M68915; GB:J05333; NID:g200471; PIDN:AAA39971.1; PID:g200472

R:Hagihara, K.; Wu-Peng, X.S.; Funabashi, T.; Kato, J.; Pfaff, D.W.

Biochem. Biophys. Res. Commun. 205, 1093-1101, 1994

A:Title: Nucleic acid sequence and DNase hypersensitive sites of the 5' region of the

A:Reference number: I49111; MUID:95100931; PMID:7802637

A:Accession: I49111

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-9 <HAG>

A:Cross-references: EMBL:U12644; NID:g639916; PIDN:AAA6067.1; PID:g639917

C:Superfamily: progesterone receptor; erba transforming protein homolog

C:Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation;

F:555-819/Domain: erba transforming protein homolog <ERBA>

F:557-577/Region: zinc finger

F:593-617/Region: zinc finger

Query Match

Best Local Similarity 21.6%; Pred. No. 1.7;

Matches 98; Conservative 52; Mismatches 177; Indels 127; Gaps 24;

QY 23 SAGIGRHLPHWNRCPPLASHTEVLPIIS-----LAAFGGSSPSQSLGVCESGTVAPVACASI 78

Db 404 SAGASSSTFFDF-----PLAPAPQAAPSSRPEGAAGVAGGSSAASPSSG-----SAL 453

QY 79 CCQVAQVFNAGSSTSWCRNPKSLPHSSIGDTRCQHLLRGSCCLVVTCLRRATTFPSPPQ 138

Db 454 ECLLYKA-----EAPTCGSFAPLPCKPPAAASCLLPRDSL-----PAAPG 494

QY 139 TSPT-----RDFALKG-PNLRIQRH-----GKVPDPWTHKMGVEGTGYNRRWVQLSGGPE 187

Db 495 TAAAPAIYQPLGNGLPQLGYQAALVLDLPPVYPYLN-----YLRPDSEASQSQF 546

QY 188 FSDLLPEARAIRVTISSGPEVSVRLCHQWALECELSSPYDVQKIVSGGHTVELPYEFL 247

Db 547 YGFDLSLQ-----KICLICGDEAG--CHYGVLTG--SKVFFKAMEGOHNY----- 591

QY 248 LPLCLCIEASYLQEDTVRRKKCP-----FQSWPEAYGSDFWKSVHFTDYS-OHTQWMA 299

Db 592 ---LCAGRNDCIVDKIRKNCACRLKCKCQAGMVLGGRKFKK--FNKVRVVRTLDGVA 645

QY 300 LTRCLPCLKEA-ALCQRHDWHTLCKLDPNATARESOGWVLEKVDLHP---QLCFKVQVP 355

Db 646 LPQSVGLPNESQALSQRITFS-----PN-----QEIQLVPPPLINLLMSIEPD 687

QY 356 FSEGNSSHVECHPQGTGSLTSWNVSMDTQAOQLILHFSRMRHATFSAAW--SLPGLGQDTL 413

Db 688 VIYAGHNTKPDTSSTLSLTSLNGERQLLSVV-----KWSKSLGFRNLHI 734

QY 414 VPPVYTVSQWVRSDVQF--AWKHLCLCPDVSYRHL 445

Db 735 DDQITLIQYSWMSLMVFLGWR-----SYKHV 761

RESULT 4

G75267

ABC transporter, permease protein, CystW family - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans


```
Db 396 CFMHRFRQACLDTCAR 412
      | : || | : | : |
RESULT 7
153280
progesterone receptor B form - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
C:Accession: I53280; B23733; A49574; A23733
R:Park, O.K.; Mayo, K.E.
Endocrinology 134, 709-718, 1994
A:Title: Regulation of the progesterone receptor gene by gonadotropins and cyclic adenos
A:Reference number: I53280; MUID:94130817; PMID:8299566
A:Accession: I53280
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-923 <PAR1>
A:Cross-references: GB:L16922; NID:G463282; PIDN:AAA19916.1; PID:G463283
R:Park, O.K.; Mayo, K.E.
Mol. Endocrinol. 5, 967-978, 1991
A:Title: Transient expression of progesterone receptor messenger RNA in ovarian granulos
A:Reference number: A23733; MUID:92049379; PMID:1840636
A:Accession: B23733
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 555-589, 'w', 591-624, 742-910 <PAR2>
A:Cross-references: GB:S64044
R:Kraus, W.L.; Montano, M.M.; Katzenellenbogen, B.S.
Mol. Endocrinol. 7, 1603-1616, 1993
A:Title: Cloning of the rat progesterone receptor gene 5'-region and identification of t
A:Reference number: A49574
A:Accession: A49574
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <KRA>
A:Cross-references: GB:S69361; NID:G546178
C:Superfamily: progesterone receptor; erba transforming protein homology
C:Keywords: DNA binding; nucleus; steroid hormone receptor; zinc finger
F:555-819/Domain: erba transforming protein homology <ERBA>
F:557-577/Region: zinc finger
F:593-617/Region: zinc finger

Query Match 3.0%; Score 105.5; DB 2; Length 923;
Best Local Similarity 21.0%; Pred. No. 7;
Matches 95; Conservative 47; Mismatches 164; Indels 147; Gaps 23;

QY 31 LPHWTRCPFLASHTEVLPISLAAPGSPSSQSLGVCESGTPAVCASTCCQVAFNGAS 90
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 418 LPPRPAPRPPRGEA---AAVAAAPAAVSP-----VSSSG-----SALEC-ILYKAEGAP 463
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 91 STSWCRNPKSLPHSSSIGDTRCOHLLRGSCCLLVVTCRLRRATFPSPQPTSTRDFALKG- 149
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 464 -----TQGSFAPLPCPKPAASCLLPRSLPAAPTSSRAPIY-PLGLNGL 510
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 150 PNLRIQRH-----GKVPFDWTHKMEVGTGYNRWVQLSGGPEFSFDLLPEAIRVTI 203
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 511 POLGYAAVLKDSLPOVYPYLN-----YLRPDSEASQSPQYGFDSLQ-----KICL 558
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 204 SSGPEVSVRLCHQWALECELSPPDVQKIVSGGHTVELPYEFLPLCLICIEASYLQEDTV 263
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 559 ICGDEASG--CHYGLVTCG--SKVFFFRAMEGQHN-----LCAGRNCDCIVDKI 604
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 264 RRKKCP-----FOSWPEAYGDFEWK-----SVHFTDYSHQTMVMA 299
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 605 RRKNCPACRLKCCQAGVGLGRKFKFNKVRMRALDGVALPQSVAPNESQ----- 657
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 300 LTLRCLKLEAALCQRDWHITLCKLDPNATARESDGWYVLEKVDLHP---QLCFKVPWF 356
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 658 -----TLGQRITES-----PN-----QEILVPPVLINLLMSIEPDV 688
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 357 SRGNSSHVECPHQTSLSWVSMDTQAQQLLHFPSSRMHATFSAW--SLPGLQDITLV 414
      || | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

```
Db 689 VYAGHDNTKPTDSSLLTSLNQLGEROLLSV-----KWSKSLPGRNLHID 735
QY 415 PPVYTSQVWRSDVQF--ANKHLLCPDVSRYHL 445
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 736 DQITLIQYSWMSLWVFLGWR-----SYKHV 761

RESULT 8
T17428
FK506 polyketide synthase - Streptomyces sp. (strain MA6548)
C:Species: Streptomyces sp.
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
A:Title: The biosynthetic gene cluster for the macrolactone ring of the immunosuppres
A:Reference number: Z18779; MUID:98451508; PMID:9780228
A:Accession: T17428
A:Status: preliminary; translated from GB/EMBL/DBJ
R:Motamedi, H.; Shafiee, A.
Eur. J. Biochem. 256, 528-534, 1998
A:Title: the biosynthetic gene cluster for the macrolactone ring of the immunosuppres
A:Reference number: Z18779; MUID:98451508; PMID:9780228
A:Accession: T17428
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-7576 <MOT>
A:Cross-references: EMBL:AF082100; NID:G3798623; PID:G3798624; PIDN:AAC68815.1
A:Experimental source: strain MA6548
C:Genetics:
A:Gene: fkbB
C:Function:
A:Description: involved in synthesis of the backbone of the immunosuppressant FK506 p
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase I homology; acetate-CoA li
C:Keywords: carrier protein
F:54-500/Domain: acetate-CoA ligase homology <ACL>
F:1095-1166/Domain: acyl carrier protein homology <ACP1>
F:1204-1599/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
F:1682-1953/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
F:2680-2751/Domain: acyl carrier protein homology <ACP2>
F:3294-3198/Domain: [acyl-carrier-protein] synthase I homology <OAS2>
F:3295-3569/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F:4320-4391/Domain: acyl carrier protein homology <ACP3>
F:4435-4830/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
F:5903-5974/Domain: acyl carrier protein homology <ACP4>
F:6018-6412/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>
F:6513-6785/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT3>
F:7450-7521/Domain: acyl carrier protein homology <ACP5>

Query Match 3.0%; Score 105.5; DB 2; Length 7576;
Best Local Similarity 20.6%; Pred. No. 84;
Matches 140; Conservative 62; Mismatches 199; Indels 279; Gaps 35;

QY 16 IVIDLSAGIGFRHLPHW-----NTRCPLASHT-----EVLPISLAAPG 55
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5190 VAVDWEVIGAAPTDPLPHTYPERTRYWLGSRAGDAAPAGOLPVAHVPLTAANVMPG 5249
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 56 -----GPSSPQSLGVCESGTPAVCASTCCQVAFNGASSTWCNRP-----KSL 101
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5250 TGDVLVLRGVEATDPLATRVNHPGAAARVLLDLRSRA---TKRAAPWRRSWTPERSAL 5306
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 102 PHSSSIGDTRCOHLLRGSCCLLVVTC-----RRATFPSPQPTSTRDFALKGNLRIQ 155
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5307 PQS-----GGLALSVTTAAPGEDGRVAVHARPGTG----- 5338
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 156 RHGKVPFDWTHKMEVGTGYNRWVQLSGGPEFSFDLLPEAIRVTISSGPEVSVRLCH 215
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5339 -----EWT-----EHATGILARVAR-----ASAVPTSPSPWPATAR--- 5371
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 216 QWALECELSPPDV-----OKIVSGGHT--VELPYEFLPLCLICIEASYLQEDTVRRKKCP 269
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5372 -----PFVDGELADRLARAGHTDGPALP-----p 5396
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 270 FQSWPEAYGDFWKSVMHFTDYSHQTMVMAITLRCPLKLEAALCQRDWHITLCKDLPNAT 329
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 5397 RAAWAD-----DDAVHAEVALA-----DEQHAD 5419
      : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 330 ARESDGWVLEKVDLHPQLCKFQVPWFSGNSSHVECP-----HOTG-----SLTS 375
```


Db 5420 A-----ERYGLHPALLGAALALAGEG-----ADLPSAFDVRVHATGATTVRVAVTA 5466
Qy 376 WNVSMDTQAOQLLHFSSRHATFSAAMSLPGLGODTL-----VPPVTYSQVMSDSYQF 430
Db 5467 TGHLEADETGSPVATGVARRRPLVEGAVPGLLRPDIAEIAELPPT-TATTTGGGLDDP-- 5523
Qy 431 ANKHLCPDV-----SYRHGLGLLILALL-ALLT---LLGVVLTALTCRRPQS 472
Db 5524 -----VVPDWWILPAHGTGGPLGETRDLGARVLAAALRSFLTDTRYADAVLAV-----HT 5573
Qy 473 GPG--PARPVLLHAADSQAORRLVCAAE-----LLRAALGGGRDVIDVLWEGRHVAR 524
Db 5574 GFLAPAAAGLVRTQAQAEHPRIIVVDAEPTAAPLAAAGLGEPOQV-LREGRAYAR 5632
Qy 525 -----VGPLWMLWAARTVRAREQGTVLLWSGADLRVSPGDPRAAPLLA---LLHAA 574
Db 5633 RLTPAVPSGDAPEL-----DPDGTVL-----ITGSGTLAGIVARHLVGHYG 5674
Qy 575 PRPLLILAYFSLCAKGDIP 594
Db 5675 VRRLLML---SRGGTASDVP 5691

RESULT 9

A83106
hypothetical protein PA4320 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

A:Accession: A83106

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen.
A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: A83106

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-523 <STO>

A:Cross-references: GB:AE004848; GB:AE004091; NID:99950537; PIDN:AAG07708.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA4320

Query Match 3.0%; Score 105; DB 2; Length 523;
Best Local Similarity 22.2%; Pred. No. 3.9;
Matches 105; Conservative 44; Mismatches 143; Indels 182; Gaps 25;

Qy 301 TLRCPLK-----LEAALCORHDWHTLCKDLP-----NATARESD 334

Db 88 TLRQALRAYPALLRKQLPASLWRRFSPTRSFDLPVLOLEGLAGEPRSORLIVLSQRNAG 147

Qy 335 GWYVLEKVDLHPQLCFKVPWFSGNSHVECPHQTSGLTSMNYSMDTQAOQLIL--HFS 392

Db 148 GATWLTVVGVHLEMA-----WAGFAMLLYLLIPAQNETDWNQSLDPEAGEWLWLEHLS 203

Qy 393 SRMHATFSAANSLPGLGODTLVPPVY-----TVSQVWRSYQFAWKHLCCPDV 440

Db 204 NLLYVLVLVWVE-----PIYVACGFTLVNRRRTELEAW--DIELVFRRL----- 245

Qy 441 SYRHGL---LLILALLALLTLGVVLTALTCRRPGCP-----ARPVLLLHAADSEARRL 494

Db 246 RORLVGSAYVLLGLTASLAWL-----PAPSAYABPA-----AATSAGEAEL 287

Qy 495 VGALAEALLRAALG---GGRDV--IVD----- 515

Db 288 PPEQARLLRQKLSNQAGKQIRIIVDGAFFNNSETVTGWRFGDKTEKKOSKDEERLKA 347

Qy 516 LWEG-----RHVARV--GPLPW-----LWAAR-----TRVAREQGT 544

Db 348 FFEALANVPRFRAQVIEVLLWALLFSAVFLVVRVREWLRLFVGNLGLPQARREAPT 407

Qy 545 VLLWSGADLRVSPGDPRAAPLLALLHAAPRPLLLAY---PSRLC-----AK 590
Db 408 VME---GLDLSPESLPDDIASNAERLWNEKPREALGLLYRGLLSRLLDYRLPLKGSHT 464
Qy 591 GDIPPPRALPRYRLRLDLPRLLRALDARFAEATSWG-RLGARQRQRSLC 643
Db 465 GEVLREGLRQORPLHYSQLTAQ-----WQALAYGHRLPADDTTRQ---RLC 510

RESULT 10

F75584

hypothetical protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000

C:Accession: F75584

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75584

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-709 <WHI>

A:Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12514.1; PID:g646

A:Experimental source: strain R1

C:Genetics:

A:Gene: DRA0305

A:Map position: 2

Query Match 3.0%; Score 104; DB 2; Length 709;
Best Local Similarity 26.2%; Pred. No. 6.6;
Matches 86; Conservative 23; Mismatches 105; Indels 114; Gaps 15;

Qy 398 TFSANSL---PGLGQDTLPPVTVYSQV-----WRS---DVQFAWKHLCLP 438

Db 297 SLTALWGLDLPSPGEGFWTPLLRLVSPALVGLAGALRAAQWRARHPHTPPLAWLAGLCG 356

Qy 439 DVSVRHGLLLALLALLTL-LGVVLTALTCRRPQSGPG-----PARPVLL----- 483

Db 357 AVLVLGDTGDTLLTLTLALSGVLAHRSALAPDLRGTLYWGPALGGLGGFLIAR 416

Qy 484 -----HAADSEAQRRLVGLAELRAAL-----GGGRDVIDLWEGRHVARVGPPLWLM 532

Db 417 AVGGGAH-----SRLLVGSILAAALTALTARQAQGGREKLGOAKLGQRTAEAGGLVLLA 472

Qy 533 AARTVAREQGTVLLWSGADLRVSPGDPRAAPLIALHAAPRPLLLLAYFSLCAKGD 592

Db 473 LALTFMAR-----PAQFAPALAL-----TALVAALLPLRVGE 505

Qy 593 IPPPLRALPRYRLRLDLPRL-----RALDARPEAEATSW-----G 628

Db 506 -----RVWLLLLGLPALAWQWLASSALWQEEANAQPLALLGAWLLLVSWLTQDDTG 558

Qy 629 R--LGAQRQRSLCRLEREAAALA 654

Db 559 RWLSLRVPARSALVL-----RRLPRLA 581

RESULT 11

JU0132

acylaminoacyl-peptidase (EC 3.4.19.1) [validated] - pig

N:Alternate names: acyl-peptide hydrolase; acylamino-acid-releasing enzyme

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 21-Jul-2000

C:Accession: JU0132

R:Mitta, M.; Asada, K.; Uchimura, Y.; Kimizuka, F.; Kato, I.; Sakiyama, F.; Tsunasawa

J. Biochem. 106, 548-551, 1989

A:Title: The primary structure of porcine liver acylamino acid-releasing enzyme deduc

A:Reference number: JU0132; MUID:90110044; PMID:2691504

A:Accession: JU0132

A:Molecule type: mRNA

A:Residues: 1-732 <MIT>

C:Genetics:

A:Introns: 4/3; 49/1; 91/2; 122/3; 148/1; 202/3; 248/3; 279/2; 293/1; 333/3; 354/1; 386/

C:Function:

A:Description: EC 3.4.19.1 [validated, MUID:90110044]

C:Superfamily: acylaminoacyl-peptidase

C:Keywords: acetylated amino end; homotetramer; hydrolase; omega peptidase

F:1/Modified site: acetylated amino end (Met) #status experimental

F:587,675,707/Active site: Ser, Asp, His #status predicted

Query Match 3.0%; Score 104; DB 1; Length 732;

Best Local Similarity 21.2%; Pred. No. 6.9;

Matches 78; Conservative 45; Mismatches 141; Indels 104; Gaps 18;

QY 136 PPTSTPTDFALKGNRIQRHGVFDPWTHKGEVGTGY--NRR-----WVQLSGGPEFS 189

DB 241 PESVSPGQAFWAPGDT-----GVVFGWHEPFRGLGIRFCTNRRSALYVVDLTGG---K 291

QY 190 FDLPEARAIRITISSGPEVSVRLC-----HMALECEELSSPYD---VQKI 233

DB 292 CELSD-ESVAVT---SPRLSPDQCRIVYLRFPISLPHQ---QCQLCL-YDWYTRVTSV 343

QY 234 V-----SGHVTVELPYBEFLPCLCEASYLQEDIVRRKKKCPFGSWPAYGS-- 279

DB 344 VVDIVPRQLGEDFGIYCSSLP---LGCWSADSQRVVFDSPQRSQDLFAVDTMGMSVT 399

QY 280 -----DFWKSVMHTDYDQHTQVMWALTLRCLKLEAALCORHWHTLCKDLNATAR 331

DB 400 SITAGSGGSMK---LLTIDRLMVFQSTPSPVPSLVKGF-----LPPAGKE 444

QY 332 ESDGVVLEKVDLPQLCFKVPWFSGNSSHVE---CPHOTGSLTWNWVSMDTQAQOLI 388

DB 445 QAVSVVLEAEAPPDIDSWIRVLQPPQOEHVQYAGLDFEAILLQPSNPEKTQVPMV 504

QY 389 LHFSSRMHATSAANSL-----PGLQDQLVPPVYVTVSQWRSVDV 428

DB 505 MPHGQ-PPHSFVTAMWLPFAMLCMKGFALLVNVYRGSTGFGQDLSLPGNVGHQDKVDV 563

QY 429 QFAWKHL 436

DB 564 QFAVEQVL 571

RESULT 12

T36882

Hypothetical protein SC151.19c - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000

C:Accession: T36882

R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A:Reference number: 221617

A:Accession: T36882

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-401 <MUR>

A:Cross-references: EMBL:AL109848; PIDN: CAB52843.1; GSPDB: GN00070; SCOEDB: SC151.19c

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB: SC151.19c

C:Superfamily: probable hexosyltransferase ytxN

Query Match 2.9%; Score 103.5; DB 2; Length 401;

Best Local Similarity 27.1%; Pred. No. 3.7;

Matches 91; Conservative 40; Mismatches 126; Indels 79; Gaps 19;

QY 356 FSGNSSHVECPHQTSWNVSMDTQAQQLILHFSRMRHATSAANSLPGLQDQLV 415

DB 79 FTGAGADHVHVRSSDPVSV--AALRTVCAEADLVHAGHLHASFRAALALG--GRVRTP 134

QY 416 PVYTVSQWV--RSDVQFAWKHLCLCPDVSRYRHLGLLILALLTLGLVVALT----- 466

DB 135 LVVT-----WHDRAHAGARGQLL--RVLERRV-----MKAATVVLGATSELVDGARRTG 182

QY 467 CRPQSGPG--PARPVLLHHAADSEARRLV-----GALAELLRAALGG-----GRDVIVD 515

DB 183 ARDARLGPVALPARPGPPAGSDDDPDLRKPVRAELGAIDRPLLVAVGSLRHRGYDVLDD 242

QY 516 ---LWEGRHVARVGPPLWMAA-----RTRVAREOGTVLLWAGADLRPVSGPDRP 563

DB 243 AARVVR-----RLDPAPLVVAVGEGPLRGELOGRIGEGPLVVLVGSRDDV-----PDLL 292

QY 564 AAPLLALLHAAPRP-----LLLAYFSRL-----CAKGDIPPLRALPRYLLRLDLPLRLRA 615

DB 293 AAADLALLLSRRPGRSVLAQEAHALHARVPLVAVAGVGIP-----ELVGDAAELVPP 343

QY 616 LDARPAEATSWGRLGARQRRQSRLELCSRLREAA 651

DB 344 GDAALADAVV--RLADPARQD--ELRERGTRQAA 375

RESULT 13

JC5598

mucin - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Nov-1999

C:Accession: JC5598

R:Inatomi, T.; Tisdale, A.S.; Zhan, Q.; Spurr-Michaud, S.; Gipson, I.K.

Biochem. Biophys. Res. Commun. 236, 789-797, 1997

A:Title: Cloning of rat Muc5AC mucin gene: Comparison of its structure and tissue dis

A:Reference number: JC5598; MUID: 97396181; PMID: 9245735

A:Accession: JC5598

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1034 <INA>

A:Cross-references: GB:U83139; NID: g2315984; PIDN: AAC53312.1; PID: g2315985

A:Note: translation not complete

C:Comment: This protein is a high molecular weight glycoprotein which is a major comp

ntestinal tract and reproductive tract.

C:Genetics:

A:Gene: Muc5A

C:Superfamily: von Willebrand factor type C repeat homology

F:45-149/Domain: cysteine-rich <CYS>

F:762-830/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 2.9%; Score 102.5; DB 2; Length 1034;

Best Local Similarity 19.1%; Pred. No. 13;

Matches 94; Conservative 43; Mismatches 168; Indels 187; Gaps 26;

QY 14 LLIVIDLSDAGIGFRHLPHWTRCPPLASHTVLPISLAAPGGSPSQ-----SL 63

DB 570 LEYASLCAGGVCIPWRSHNTNTCTPTCPEN---QVQPCGSPSNPHYCYRNDLISLSL 625

QY 64 GVCESGTVPAVCAASICCOVAQVFNQ-----ASSTSWCRNPKSLP-----HSSST----- 107

DB 626 AIQKAPKSEGC--FCPDDMTLFPSSNDSICVPSCQWCLGPHGEFVPGHTISINCCDCIC 683

QY 108 --GTRCQHLL-----RGSCCLVVTCLRRATITPSP---PQISPTPR 143

DB 684 KEGTLTCEQKLCQPCTCEPGFVPSVIALEAGQCQSOFSCVCSNSSHCPPLHCPSSSL- 742

QY 144 DFALKGNLRIQRHGVFPDW---THKGMV-GTGYNRRVQLSGGPEFSFDLLPEARAI 199

DB 743 -----IVTEGTCPCSONCCKGCDVNGTLY----- 770

QY 200 RVTISSGPEVSVRLCHQ-----WALECE-ELSS---PYDVQKIVSGGHTVEL 242

DB 771 ---QPGDVVSSSLCERCLCEVSSNAFSDVFNCEITELCNTCPKGFYQTTTGH--- 822

QY 243 PYELLPLCL--CTEASVQLQEDTVRRKKCPQSWPEATG----SDFWKS-----VFYTDY 290

DB 823 -----CCGQCVP-----KTCPEKSNNSNLSLYKPGFEWPEPGNCPVTHKCEK 864

QY 291 SOHTQVMWALTLCPLKLEAALCORHWHHTLCKD-----LPNATARSQDGVVLEKVD 343

DB 865 FQDVLTVTVTKIECP-KINCP---QDWAQLREDGCCYDCLVFQ-----QKCT 907

QY 344 LHP-OLCFKVPWFSGNSHVECPHOTGSLTSWN-----VSMDTQAQOLI 388
Db 908 VHQROOIRQNCSEGPVSLSYCGNGDSTSMYSLANVEHTCECCQELQTSQSVT 967
QY 389 LHFSSRMHATFS 400
Db 968 LHCDDGSSRTFS 979

RESULT 14

B45266

MPL-K protein precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999

C:Accession: B45266

R.Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, S.

Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992

A:Title: Molecular cloning and characterization of MPL, the human homolog of the v-mpl c

A:Reference number: A45266; MUID:92302297; PMID:1608974

A:Accession: B45266

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-579 <VIG>

A:Cross-references: GB:M90103; NID:g184262; PIDN:AAA69972.1; PID:g184263

Query Match 2.9%; Score 102; DB 2; Length 579;
Best Local Similarity 18.1%; Pred. No. 7.4; Indels 251; Gaps 29;
Matches 96; Conservative 53; Mismatches 131;

QY 31 LPHMNR-CPLASHEV---LPI-----SLAAGGSPSSPSISLG 64

Db 84 MPHECTRYVCOFPDQEEVRLFFPLHLWKNVFNLTQTRQVLFVDSVGLPAPPISIRAMG 143

QY 65 VCESGTVPAVCASICCAQVAFNGASSTW-----CRNPKSLPHSS 106

Db 144 ---GSQP-----GELQISWEEPAPEISDFLRYELRYGPRDPK-----NS 179

QY 107 IGDTRCOHLRGSCCLVY-----TCLRRATF-PSPQTSPTRD---FALKGP 150

Db 180 TGPVLIQIATETCPALQPHSASALDQSCAQPTMPWQGPQKQTSRREASALTAEKG 239

QY 151 NLRIQRHGVFPDTHKMEVGTGYNRRWVQSGGPEFSFDLLPEAIRVITSSGPEVS 210

Db 240 SCLI-----SLQPGNSY---WLQLRSEPD-----GISLGSGW 270

QY 211 VRLCHWALECEELSSPDVQKIVSGGHTVELPYE-----FLPLCLCTEASTLQEDT 262

Db 271 ---SWSLPV-----TVDLPGDAVALGQCFTLDLKNVTCQWQOQDH 308

QY 263 V-----RRKKCPQSWP----- 274

Db 309 ASSQGFYHSRACCPDRYPIWENCEEETNPGLOTQPSRCHFKSRNDSIITHILEV 368

QY 275 ---BAY-GSDPW-----KSVHFTDYSOHTQMWALTLRCPKLKLEALCORHD 317

Db 369 TPAGTVHSYLGSPFWIHOAVRLPTPNLHWEISSG-----HLELEWQHPS 415

QY 318 W-HPLCKDLNPATARESDGWVLE-----KVDLHPQLCFKQV-----PW 355

Db 416 WAAQETCYQL-RYTGEGHQDKVLEPLGARGGTLELRPRSRYRLQLRARLNGPTYGQW 474

QY 356 FSGNSSHVECPHOTGSLTSNNVSMDTQAQOLIILHFSRMHATFSAAWSLP 406

Db 475 SWSDPTRVE---TATETAW-ISLVT-ALHLVLGLSAVL-GLLLLRQFP 518

RESULT 15

B96640

hypoetical protein T25B24.15 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: B96640

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: B96640

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-829 <STO>

A:Cross-references: GB:AE005173; NID:g4585885; PIDN:AAD5558.1; GSPDB:GN00141

C:Genetics:

A:Gene: T25B24.15

A:Map position: 1

C:Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot

Query Match 2.9%; Score 102; DB 2; Length 829;
Best Local Similarity 19.5%; Pred. No. 11;
Matches 121; Conservative 64; Mismatches 165; Indels 270; Gaps 34;

QY 4 SRLAALLPLLLIVLDSAGIGFRHLPHWNTTCP-----LASHEVLPISLAAPGGP 57

Db 3 TRFACHLFTMFLTLSSGSSAVI-----TTESPLSMGOTLSANAYELGFFSPNN- 55

QY 58 SSPQSLGVCESGTVPAVCASICCAQV-----ENGASSTSW----- 94

Db 56 TQQYGVGIMFKDIPRVVWVANREXPVDTSTAYLAISSGSLLLNGRKGTVWSSGVF 115

QY 95 ---CR-----NPKSLPHSS-----IGDTRCOHLRGSCCL---VVTCLRAIT 132

Db 116 SSGCRAELSDSGNLKVIDNVSERALWQSPDHLGDT---LLTSSLTYNLATAERVL 171

QY 133 F-----PSP-----PQTSPTROPALK-----GNLRIQRHGVFPDTHKG-- 168

Db 172 SWSKYTDPSGDFGLQITPQV-PSQGFVMRGSPYWRSGPWAKTRFTGPFMDSEYTGPF 230

QY 169 ---MEV-GTG---YNRRWVQSGGPEFSFDLLPEAIRVITSSGPEVSVRLCHWALEC 221

Db 231 TLHQDVNGSGLYTFQRDYKLS-----RITLS---EGSIKMF----- 266

QY 222 EELSSPDVQKIVSGGHTVELPYEFLPLCLCTEASTLQEDTVRRKKCPQSWPEAYGSDP 281

Db 267 ---DNGMGWELYE-----APKLCDFYAGCGPFG--- 293

QY 282 WKSVMHFTDYSOHTQMWALTLRC-----PLKLEALCORHDW-----HTLCKDLPNA 328

Db 294 ---LCVNSPSPMCKCFRGFPVKSVEE---WKRGNWTCGCVRHTELDCLGNS 338

QY 329 TARESDGWVLEKVDLHPQLCFKVPWFSEFNS-----SHVECPHOTGSLT----- 374

Db 339 TGEDAD-----DFHQIANIKPPDFEPASSVNAEECHQRCVHNCSCLAFAIKIGIC 390

QY 375 -SNVSMDTQAQOLIILHFSRMHATFSAAWSLPL-----GQDTLVPVP----- 417

Db 391 LVNQDLMDAVQ-----FSATGELLSIRLARSELDGNNRKRKTIVASIVSLTL 437

QY 418 ---YTVSOVWRSDYQFANKHLCLCPDVSYRHGLLILALLA---LLTLGVVLALTCRR- 469

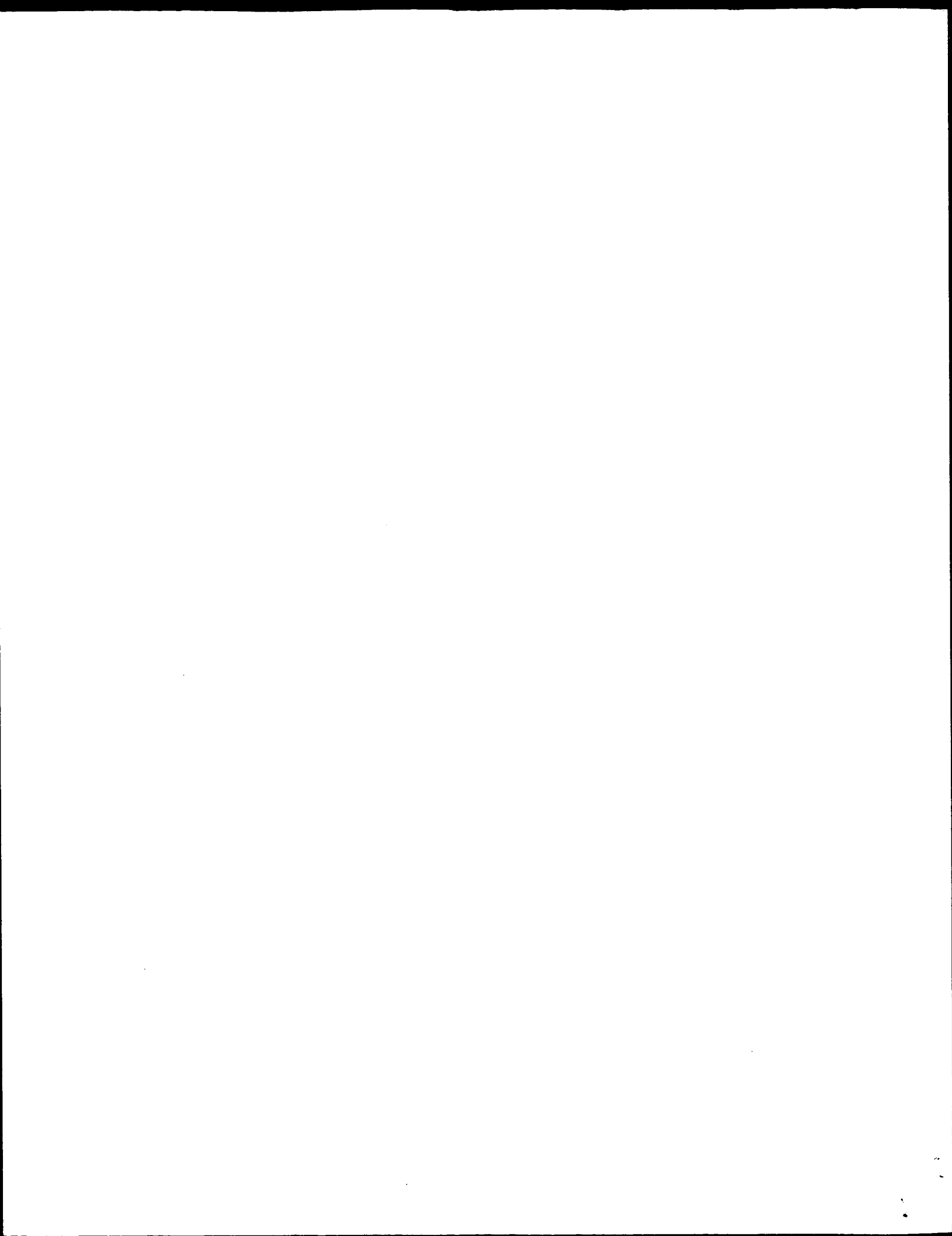
Db 438 FMILGTFAGVWRCRVE-----HIGNILMTLLSNDLLLFN---SFAKRRK 480

QY 470 -----PQSGPG 475

Db 481 KAHISKDANKDLKPDQVPG 500

Search completed: January 28, 2003, 09:30:58

Job time : 32 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:23:03 ; Search time 15 seconds
(without alignments)
1816.663 Million cell updates/sec

Title: US-09-863-818A-12

Perfect score: 3512

Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLECSRLEREAARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	126	3.6	866	1 I17R_HUMAN	Q96f46 homo sapien
2	125.5	3.6	1115	1 TBC2_CHLRE	Q8vxp3 chlamydomon
3	122	3.5	738	1 I12R_MOUSE	Q60837 mus musculus
4	121.5	3.5	864	1 I17R_MOUSE	Q60943 mus musculus
5	114.5	3.3	635	1 TPOR_HUMAN	P40238 homo sapien
6	113.5	3.2	923	1 PRGR_MOUSE	Q00175 mus musculus
7	113.5	3.2	1199	1 Y173_HUMAN	Q14679 homo sapien
8	107.5	3.1	452	1 GASR_RAT	P30553 rattus norv
9	105.5	3.0	923	1 PRGR_RAT	Q63449 rattus norv
10	104	3.0	732	1 ACPH_PIG	P19205 sus scrofa
11	104	3.0	1202	1 JAG2_RAT	P97607 rattus norv
12	104	3.0	1247	1 JAG2_MOUSE	Q9qy65 mus musculus
13	102	2.9	930	1 PRGR_RABIT	P06186 oryctolagus
14	101.5	2.9	1088	1 PIGO_HUMAN	Q8teq8 homo sapien
15	100.5	2.9	685	1 FHUB_SALTY	O87656 salmonella
16	100	2.8	1193	1 BCHK_RHOSH	O9rfd5 rhodobacter
17	99.5	2.8	1093	1 PIGO_MOUSE	Q9jjj6 mus musculus
18	99.5	2.8	1435	1 Y194_HUMAN	Q12766 homo sapien
19	99	2.8	453	1 GASR_MOUSE	P56481 mus musculus
20	98	2.8	732	1 ACPH_RAT	P13676 rattus norv
21	97.5	2.8	316	1 UNG_PVKRA	P52507 pseudorabie
22	97.5	2.8	452	1 GASR_RABIT	P46627 oryctolagus
23	96.5	2.7	948	1 CHRD_MOUSE	Q9z0e2 mus musculus
24	96.5	2.7	1964	1 NTCA_MOUSE	F31695 mus musculus
25	95.5	2.7	2205	1 POLN_RUBVT	P13889 rubella vir
26	95	2.7	396	1 CYB_PETMA	Q35534 petromyzon
27	95	2.7	453	1 GASR_CANFA	P30552 canis famil
28	94.5	2.7	955	1 CHRD_HUMAN	O9h2x0 homo sapien
29	94	2.7	657	1 DCTS_RHOCA	P37739 rhodobacter
30	93.5	2.7	761	1 PQQE_KLEPN	P27508 klebsiella
31	93.5	2.7	910	1 DDRI_RAT	Q63474 rattus norv
32	93.5	2.7	3718	1 LMA5_MOUSE	O61001 mus musculus
33	93	2.6	573	1 AMH2_HUMAN	Q16671 homo sapien

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34      93      2.6      1238      1      JAG2_HUMAN      Q9y219 homo sapien
35      92.5      2.6      491      1      A2AF_HUMAN      P08697 homo sapien
36      92.5      2.6      513      1      ENV_BLV82      P25506 bovine leuk
37      92.5      2.6      515      1      ENV_BLV85      P25507 bovine leuk
38      92.5      2.6      555      1      MIS_MOUSE      P27106 mus musculus
39      92.5      2.6      665      1      DUSX_HUMAN      Q9by84 homo sapien
40      92.5      2.6      795      1      DEGY_CAEEL      O01635 caenorhabdi
41      92.5      2.6      2144      1      CLR2_RAT      Q9gyp2 rattus norv
42      92      2.6      1246      1      SKIW_HUMAN      Q15477 homo sapien
43      92      2.6      2003      1      NTC4_HMOCA      Q99466 homo sapien
44      91.5      2.6      294      1      HUPK_RHOCA      P30797 rhodobacter
45      91.5      2.6      933      1      PRGR_HUMAN      P06401 homo sapien

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ALIGNMENTS

RESULT 1

```

I17R_HUMAN
ID      I17R_HUMAN      STANDARD;      PRT;      866 AA.
AC      Q96f46; O43044;
DT      15-JUN-2002 (Rel. 41, Created)
DT      15-JUN-2002 (Rel. 41, Last sequence update)
DE      Interleukin-17 receptor precursor (IL-17 receptor).
GN      IL17R.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=T-cell;
RX      MEDLINE=98035683; PubMed=9367539;
RA      Yao Z., Spriggs M.K., Derry J.M.J., Strockbine L., Park L.S.,
RA      VandenBos T., Zappone J., Painter S.L., Armitage R.J.;
RT      "Molecular characterization of the human interleukin (IL)-17
RT      receptor."
RL      Cytokine 9:794-800(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Uterus;
RA      Strausberg R.;
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC      -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC      suggesting that additional components are involved in IL17-induced
CC      signaling.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC      -!- TISSUE SPECIFICITY: Widely expressed.
CC      -!- PTM: Glycosylated.

```

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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR      EMBL; U58917; AAB99730.1; -.
DR      EMBL; BC011624; AAH11624.1; -.
DR      Genew; HGNC:5985; IL17R.
DR      MIM; 605461; -.
KW      Receptor; Transmembrane; Signal; Glycoprotein.
FT      SIGNAL      1..31
FT      CHAIN      32..866
FT      DOMAIN      321..320
FT      TRANSMEM      321..341
FT      DOMAIN      342..866
FT      CYTOPLASMIC      810..818
FT      CARBOHYD      49..49
FT      CARBOHYD      54..54
FT      CARBOHYD      206..206

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FT CARBOHYD 225 225 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 242 242 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLNAC. . .) (POTENTIAL).
FT CONFLICT 367 367 V -> A (IN REF. 1).
FT CONFLICT 580 580 H -> R (IN REF. 1).
SQ SEQUENCE 866 AA; 96131 MW; 28330BED2303B0C9 CRC64;

Query Match 3.6%; Score 126; DB 1; Length 866;
Best Local Similarity 18.4%; Pred. No. 0.069;
Matches 108; Conservative 75; Mismatches 197; Indels 206; Gaps 26;

Qy 116 LRSGCLVVTCLRAITFPSPQSPTRDFALKGNRIQRH-----GKVP-----DWT 165
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 52 VKNSTCLDDSHINPLNTPSPK-----DLQIQHFAHTQOGLFPVAHIEWT 99
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 166 -----HKMEVGT-----GYNRRWQVLSGGPEFSDLLPEA 196
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 100 LQDASILYLGAEVLSVLQNLNTRLCVRFFELSKLHHHRW-----RFTFS----- 147
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 197 RAIKRTISSGSEVRLCHQWALECEELSSPDYQKIVSGGHTVELPYEFILP----- 249
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 148 ---HEVDPDQOYEYVHH-----LPKPIPDGDPNHQSKNFIPLVPCDEHARM 190
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 250 ---CLCIEASYLQEDTV-----RRKKCPQSPWPEAYGDFWKSVEHFTDYQSHTQWMA 299
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 KVTTPCMSGSLWDPNITVETLEAHQLRVSTPLWNE-----STHYQIILLT 235
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 300 LTRCPKLEALCORHWHHTLCKDLNATARESDGVVLEKVDLHPQLCFKVPWF-- 357
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 ---SFP-HMEHNSCFEH-MHHIPAPREEFHORSNVITLNLKGGCRHQVQIQPFSSC 290
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 358 ---FGNSHVECHQPTGS-----LTSWNVSMQTAQQLILHFSSRMHATFSAANSLP 406
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 LNDCLRHSAVSCPEMPDTPPEIDYPLWYWFITGIS--ILLVGSVILLIVCMTWRLA 348
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 407 GLGQDTLPVPVYVYQVWRSVDQFAWKHLCPDVSYRHLGLLILALLALLTLGVLVALT 466
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 GPG-----SEKYSDDTKYT-----DGLPVADLI----- 371
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 467 CRRPQSGPGRP--VLLHHAADSEAQRRLYALAEALLRAALGGGRDVIDVLWEGRHVAR 524
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 372 -----PPPKPRKVKVYISADHPLVYDVVVKFAQFLITAC--GTEVALDLLEQAISE 422
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 525 VGPLPWLWAARTVAREOGTVLLWS-----GADLR-----PVSGDPDPA 564
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 423 AGVMTWVGROQEMVESKIIVLCSRCTRAKQWQALLGRGAPVRLRCDHGKPGV--DLFT 480
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 565 APLALLHAARP-----LILLAYSRLCAKGDIPPPRALPRYRL 606
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 481 AAMNMILPDKRPACFGTYVYVYVYSEVSCDGDVDPDLFGAAPRYPLM 526
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
TBC2_CHLRE
ID TBC2_CHLRE STANDARD; PRT; 1115 AA.
AC Q8VXP3;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tbc2 translation factor, chloroplast precursor.
GN TBC2.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=137c / CC-125;
RX PubMed=12045185;
RA Auchincloss A.H., Zerges W., Perron K., Girard-Bascou J.,
RA Rochaix J.-D.;
RT "Characterization of Tbc2 a nucleus-encoded factor specifically
RT required for translation of the chloroplast psbC mRNA in
```

Db 575 GEVALSLNALGRL--SAVMDLPLALIDLMSGRVLDLTSRLAAGFGSGGLQLLEGLT 632
 QY 449 ILAL-----LALLTLGLVGLALTCRRPQSGPARGPVLILLHAADS 488
 Db 633 RLALQPLEWMAQFAALQPLDKLDAQGLVLSLAQ--QYRQPMQEWVLAATQA 690
 QY 489 E-----AQRL-----VGALAEALLRAALGGGRDVIDLVGEGRHVAR 524
 Db 691 NMKQLLADTCSAALLTALRLNLEPPPGWVGALLEERSAL---KNRCTDL---HLAN 743
 QY 525 V-GPL-PW-----LWAARTVAREQGVTVLLWSCADLRPVSGPPRAAPLALLHA--- 573
 Db 744 LAGSLAAGVRPDGWAAR-----LMWRSQVLNEDRMSRA--LVALIQAMVS 790
 QY 574 ---APRPLLLAYFSLCAK-----GDIPPLRAL-----PRYLLRLDLP 610
 Db 791 LGLSPNV-----WTQLCLQAVRASQAPPEPHYGTMLASLHAGLQPPQEWLTRLML 845
 QY 611 RLLRALDARPAEATSWGR-----LGARQRQ--SRLELCSRLEREAAARLAD 655
 Db 846 STYRCWDR---FSVTHSSLLPALVLLKARPPREWLRFEATS-----AARLAD 891

RESULT 3
 IL12R_MOUSE
 ID IL12R_MOUSE STANDARD; PRT; 738 AA.
 AC Q60837;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-12 receptor beta-1 chain precursor (IL-12R-beta1)
 (Interleukin-12 receptor beta) (IL-12 receptor beta component).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=96025887; PubMed=7594587;
 RA Chua A.O., Wilkison V.L., Presky D.H., Gubler U.;
 RT "Cloning and characterization of a mouse IL-12 receptor-beta
 component.";
 RL J. Immunol. 155:4286-4294 (1995).
 RN [2]
 RP SUBUNIT
 RX MEDLINE=97098510; PubMed=8943050;
 RA Presky D.H., Yang H., Minetti L.J., Chua A.O., Nabavi N., Wu C.-Y.,
 RA Gately M.K., Gubler U.;
 RT "A functional interleukin 12 receptor complex is composed of two
 beta-type cytokine receptor subunits.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14002-14007 (1996).
 CC -1- FUNCTION: INVOLVED IN IL-12 TRANSDUCTION. BINDS TO IL-12 WITH A
 LOW AFFINITY.
 CC -1- SUBUNIT: DIMER/OLIGOMER; DISULFIDE-LINKED. THE FUNCTIONAL HIGH
 AFFINITY IL-12 RECEPTOR IS COMPOSED OF AT LEAST IL12RB1 AND
 IL12RB2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
 CC -1- SIMILARITY: CONTAINS 5 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U23922; AAA87457.1; -;
 DR MGI:104579; IL12RB1.
 DR InterPro: IPR003961; FN_III.

DR InterPro: IPR003529; Hemtopoptn_L_F2.
 DR Pfam: PF00041; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01353; HEMATOPO_REC_L_F2; FALSE_NEG.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 738 INTERLEUKIN-12 RECEPTOR BETA-1 CHAIN.
 FT DOMAIN 20 565 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 566 591 POTENTIAL.
 FT DOMAIN 592 738 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 142 142 FIBRONECTIN TYPE-III 1.
 FT DOMAIN 152 258 FIBRONECTIN TYPE-III 2.
 FT DOMAIN 259 359 FIBRONECTIN TYPE-III 3.
 FT DOMAIN 360 465 FIBRONECTIN TYPE-III 4.
 FT DOMAIN 467 553 FIBRONECTIN TYPE-III 5.
 FT DISULFID 53 63 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 130 130 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 330 330 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 368 368 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 401 401 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 477 477 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 738 AA; 81661 MW; 05D7AC306F1059CE CRC64;
 Query Match 3.5%; Score 122; DB 1; Length 738;
 Best Local Similarity 20.3%; Pred. No. 0.11;
 Matches 128; Conservative 61; Mismatches 183; Indels 260; Gaps 36;
 QY 38 CPLASHTVEPLPI-----SLAAPGPGSSPQSLGVCSTGTPAVCAVSCCQVAVFGASS 91
 Db 218 CPSENMAQEIQIRRRRLSSGAPGPGWDSMPVC---VP----- 254
 QY 92 TSWCRNPKSLPHSSSGDTRCQHLRGSCCLVVTCLRRATF--PSPPTSPTRDFALKG 149
 Db 255 -----PEVLPOAKI--KFLVEPLNQG-----RRRLTMQGSQPLAVPE---GCRG 295
 QY 150 -PNLRIQRHGKVF-----PDWTHKGMEVGTGYNRRWQLSGGPFESDPLPEAIRV 201
 Db 296 RPAQVAKHLVLRMLSCRCQAQTSKTVPGLKKLN-----LSGA-TYDLNLAKTRFGRS 349
 QY 202 TISSGPEVSVRLCHQWALECEELSSPYDVQKIVSGGHTVELPYEFLP--CLCIEASYLQ 259
 Db 350 TI-----QKWLHPAQELTETRALNVSV-GGNMTSMQWAAQAPGTYTCLE----- 392
 QY 260 EDIVRRKKCFQSWPEAYGSDFWKSVHFTDYSOHTQVMALTRCPLKLEAALCQRDWH 319
 Db 393 -----WQPV-----FQHRNHTH---CTLIVPEEDPAKMWTHWS 424
 QY 320 TLCKDLPNATARESDGWYV---LEKVDLHPQLCFKQVPWFSEGNSS-----HVECPHQ 369
 Db 425 S-----KPTLEQECYRITVFASKNPKNPKMLWATVLSSTYFGGNASRAGTPRHVSVRNQ 478
 QY 370 TGSILTS--WNVSDMTQAOQLILHFSRRMHTATFSAANSLPGLGQDTLVPPVTVTSQV--- 423
 Db 479 TGDVSVSEVETASQLSTCPGVLTQVYVVRCEAE-DGANE-----SEWLVP--TKQTVDLG 530
 QY 424 WRSDVOF-----AWKHLICP-----DVSYRHIGLLILAL-----LALLTLIG 460
 Db 531 LRSRVMYKQVADRATRLPGAWSH---PQRFSEVQISRLSIIFASIGSFASVLLVGSIG 587
 QY 461 VW-----LALTC----- 467
 Db 588 YIGLNRAWHLCPPPLTPCGSTAVEPFGSGQKQAWQMCNPEDPPEVLYPRDALVWEMPGD 647
 QY 468 -----RRPQSGPGPA-----RPVLLHAADEAQR--RLVGALAEALLRAA----- 505

```

Db 648 RDGTSPQAAPEACALDRRL-----ETQRQRQVQALSEARRLGLAREDCPRGDLA 699
QY 506 -----LGG---GRDIVDLWEGRHVARVGP 527
Db 700 HVTLPILGGVTOGASVLDLDRTHKTAEPGP 731

RESULT 4
ID IL17_MOUSE STANDARD; PRT; 864 AA.
AC Q60943;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-17 receptor precursor (IL-17 receptor).
GN IL17R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymic lymphoma;
RX MEDLINE=96111968; PubMed=8777726;
RA Yao Z., Fanslow W.C., Seldin M.F., Rousseau A.M., Painter S.L.,
RA Comeau M.R., Cohen J.I., Spriggs M.K.;
RT "Herpesvirus Saimiri encodes a new cytokine, IL-17, which binds to a
RT novel cytokine receptor.";
RL Immunity 3:811-821(1995).
CC -!- FUNCTION: Receptor for IL17. Binds its ligand with low affinity,
CC suggesting that additional components are involved in IL17-induced
CC signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U31993; AAC52357.1; -.
DR MGD; MGI:107399; Il17r.
KW Receptor; Transmembrane; Signal; Glycoprotein.
FT SIGNAL 1 31
FT CHAIN 32 864
FT DOMAIN 32 322
FT TRANSMEM 323 343
FT DOMAIN 344 864
FT DOMAIN 809 814
FT CARBOHYD 54 54
FT CARBOHYD 79 79
FT CARBOHYD 206 206
FT CARBOHYD 225 225
FT CARBOHYD 242 242
FT CARBOHYD 265 265
FT CARBOHYD 308 308
FT CARBOHYD 308 308
SQ SEQUENCE 864 AA; 97807 MW; 343FD51AA687DA31 CRC64;

Query Match 3.5%; Score 121.5; DB 1; Length 864;
Best Local Similarity 17.5%; Pred. No. 0.15;
Matches 118; Conservative 97; Mismatches 182; Indels 277; Gaps 33;

QY 46 VLPISLAAGPSSQSLGVCESGVPA-VCA--SICCOVAQVFNAGSSTWCNRPKSLP 102
Db 20 LLLNLVAP-GRASPRLL-----DFPAPCAQEGLSRVN--STCLDDSWI-HPNLT 69
QY 103 HSSSIDGTRCOHLRGSCCLVVTCLRRAITPPSPPTPTDFALKGNLRQ--RHGKV 160
Db 70 -----PSSPKNIYI-----NLSVSTQHGL 90
QY 161 FP-----DWT-----HKGEVCT-----GYNRRWVQLSGGP 187

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Db 91 VVPLHVWETLQTDASILYLEGAELSVLQNLNRLCKVQFQLSMLOHHRKW-----R 143
QY 188 FSDLLPEARAIRVTISSPEVSVRLCHQ-----WALCEELSSPYDVQ 231
Db 144 FSPS-----HFVDPGQGEYEVTVHILPKPIPDGDPNHKSLIFVPCDESKMKMTTS 195
QY 232 KIVSG-----GHTVELPYEFLPCLCLTEASYLOED-TVRRKKCPQFQSWPEAYGSDFWKSV 285
Db 196 CVSSGSLWDPNIIVE-----TLDQHLRVDTFLNNESTPYQVLLS----- 236
QY 286 HFTDYSOHTOMWMLTLRPLKLEAALCORHWHLTCKDLPNATARESDGWTVLEKVDLH 345
Db 237 -FSDSENHSCFDVVKQIFAP-----RQEEPH-----QRANVTFTLSKFHW 276
QY 346 POLCFKVPWFES-----FGNSSHVPCPQHOTGLSTSMNVSMDTQAQQLILHFSRHMATF 399
Db 277 CHHHVQVQPFSSCLNDLKHAVTVCP----- 304
QY 400 SAASWLPGLGQDTLPV-PVYTVSQVWRSDVQFAWKHLLCPDVSYRHLGLL-LTALLALT 457
Db 305 -----VISNTVPKPVADYIPLW-----VYGLTILAILLVGS 337
QY 458 LLGVVIALTCR-----RPSQG-----PGPARP-VLLLHAADSEAOORLV 495
Db 338 VIVLLICMTWRLSGADQEKHDDSKINGILPVADLTPLPRKRWIVYSADHPIYVEV 397
QY 496 GALAEILLRGAALGGRDVIVDLWEGRHVARVGPPLPWAARTVAREQGVLLWS---GA 552
Db 398 LKFAQELITAC--GTEVALDLEEQVISEGVWTVWSROKQWESNKKIILCSRGTOA 455
QY 553 DLRPVSG-----PDRAAPLALLHAAPRP-----LLLAYFSRLCAKGD 592
Db 456 KWAILGWAEPVOLRCDHMKPAGDLFTAAMNMLPDFKRPACFGTVVVCYFSGICSERD 515
QY 593 IPPPLRALPYRL 606
Db 516 VPDLFNITSRYPLM 529

RESULT 5
TPOR_HUMAN STANDARD; PRT; 635 AA.
ID TPOR_HUMAN
AC P40238;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia
DE protein) (C-mpl) (CD110 antigen).
GN MPL OR TPOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92302297; PubMed=1608974;
RA Vigon I., Mornon J.-P., Cocault L., Mitjavila M.-T., Tambourin P.,
RA Gisselbrecht S., Souvri M.;
RT "Molecular cloning and characterization of MPL, the human homolog of
RT the v-mpl oncogene: identification of a member of the hematopoietic
RT growth factor receptor superfamily.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292186; PubMed=8020956;
RA Mignotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
RA Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
CC -!- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

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CC NR3 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M68915; AAA39971.1; -.
DR EMBL; U12644; AAA66067.1; -.
DR PIR; A39596; A39596.
DR HSSP; P06401; IA28.
DR TRANSFAC; T04680; -.
DR MGD; MGI:97567; Pqr.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR000128; Progesterone_receptor.
DR Pfam; PF001628; Znf_C4steroid.
DR Pfam; PF00105; zf-C4; 1.
DR Pfam; PF02161; Prog_receptor; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger; Steroid-binding.
FT DOMAIN 1 556 MODULATING, PRO-RICH.
FT DNA_BIND 557 622 NUCLEAR RECEPTOR-TYPE.
FT ZN_FING 557 577 C4-TYPE.
FT ZN_FING 593 617 C4-TYPE.
FT DOMAIN 671 923 STEROID-BINDING.
FT DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 923 AA; 99073 MW; 9415FIED343BEE3F CRC64;

Query Match 3.2%; Score 113.5; DB 1; Length 923;
Best Local Similarity 21.6%; Pred. No. 0.66;
Matches 98; Conservative 52; Mismatches 177; Indels 127; Gaps 24;

QY 23 SAGIGFRHLPHNTRCPPLASHTVEVLPIS-----LAAPGGSSPQSLGVCESGTVPAVCASI 78
DB 404 SAGASSTTFDP-----PLAPAPQAPSSRPGAEAVAGGSSAAVSPASSG-----SAL 453
QY 79 CQQAQVFNAGSSTSWCRNPKSLPHSSSTGTRCQHLRLSGCCLVVTCLRRAITPPSPQ 138
DB 454 ECILYKA-----EAPPTQGSFAPLPCKPPAAASCLLPDRSL-----PAAPG 494
QY 139 TSPT-----RDFALKG-PNLRIOQH-----GKVPDWTGKMEVGTGYNRRWVQLSGGPE 187
DB 495 TAAAPAIYQPLGLNLPQLGYQAAVLKDSLPPQVPPYLN-----YLRPDSEASQSPQ 546
QY 188 FSDLLPEARAIRVTISSGPEVSRVLRCHOWALECEBELSPYDVOKIVSGGHTVELPYEFL 247
DB 547 YGFDSLFP-----KICLICDEASG-CHVGVLTCG-SCKVFFKRAMGQNNY----- 591
QY 248 LPLCLTEASYLOEDTVRRKKCP-----FQSWPEAYSGDFWKSVFHFTDYS-QHTQMVMA 299
DB 592 ---LCAGRNDICVDIKRKNCFACRLRCKCQAGMVLGGRKFKK-----FNKVRVMRTLDGVA 645
QY 300 LYLRCPLKLEA-ALCQRHDWHTLCKDLNPATARESDGWVLEKVDLHP---QLCFKQVOPW 355
DB 646 LPQSVGLPNESQALSQRITFS-----PN-----QEIOLVPPPLNLLMSIEPD 687
QY 356 FSEGNSSHVCEPQGTSLTSWVSMYMDTQAQQLLHFSRMRHATFSAW-SILPGLGQDQL 413
DB 688 VIYAGHDNTKPDTSLSLTSLNQLGERLLSVV-----KWSKSLPGERNLHI 734
QY 414 VPPVTVSQVRSRDVQF--AWKHLLCPDVSRYHL 445
DB 735 DQOITLIQYSWNSLMVFLGLWR-----SYKHV 761

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RESULT 7
Y173 HUMAN
ID Y173_HUMAN STANDARD; PRT; 1199 AA.
AC Q14679;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein KIAA0173.
GN KIAA0173.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE=96281124; PubMed=8724849;
RA Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. V.
RT The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 3:17-24(1996).
CC -1- SIMILARITY: CONTAINS 1 TTL DOMAIN.
CC -----
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CC -----
DR EMBL; D79995; BAA11490.1; -.
DR InterPro; IPR004344; Tub_tyr_lyase.
DR Pfam; PF03133; TTL; 1.
KW Hypothetical protein; Polymorphism.
FT DOMAIN 651 946 TTL.
FT VARIANT 418 418 R->H (IN DBSNP:2114664).
FT SEQUENCE 1199 AA; 133376 MW; 5306D5FA37431081 CRC64;

Query Match 3.2%; Score 113.5; DB 1; Length 1199;
Best Local Similarity 18.4%; Pred. No. 0.9;
Matches 102; Conservative 68; Mismatches 175; Indels 209; Gaps 27;

QY 16 IVIDLSDSAGIGFRHLPHNTRCPPLASHTVEVLPISLAAPG---GPSSPQSLGVCESGTVP 72
DB 419 ISHLLASHASGLNH-----NPAC-----ESVIDSSAFGECKAPGPPPTLGI----- 462
QY 73 AVCASICQQAQVFNAGSSTSWCRNPKSLPHS-----
DB 463 ---ANVATRLSSILGQSEKERPEARELSDSDISSATDLPDQAEATEDTEELVDGL 519
QY 105 -----SSIGDTRCOHL-----LRGSCLVVT-----CLRRATFPS 135
DB 520 EDCSREDNEEEGDSECSLSAVSPSESVAMISRSCEILTKPLSNHKEKVRPALIYL 579
QY 136 PPOTSPTDRFA-----
DB 580 FPNVPTIYGTDRDERVEKLPWEQRKLLRWKMSIVTPNIVKQITGRSHFKISKRNDDWL 639
QY 147 -----LKGPNLR-IQRHGKV--FPDWTGKMEVGTGYNRRWVOLS-----GGPEFSF-- 190
DB 640 CWGHMKSPSFRSIREHQKLNHPG-----SFQIGR-KDRLWRNLRSRQSRFGKKEFSFP 694
QY 191 --DLLP-EARAIRVTISSGPE-----VSRLCHOWA-----LECEBELSS 226
DB 695 QSFILPDQAKLLRKAWESSSRQKWIWKPPASARGIGIQVTHKWSQLPKRRPLLVQRYLHK 754
QY 227 PYDVQKIVSGGHTVELPYEFLPLCLCIEASY-----LOEDTVRRKKKCPQSWPEAYGS 279
DB 755 PY-----LISGS-----KFDLRIYVYVTSYDPLRIYLFSDGLVRFASCKYSPSMKSLGN 803

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CC	EMBL: L16922; AAA19916.1; -	
DR	HSP; P06401; 1A28.	
DR	TRANSFAC; T04681; -	
DR	InterPro; IPR000536; Hormone_rec_lig.	
DR	InterPro; IPR000128; Progester_receptor.	
DR	InterPro; IPR001628; znf_C4steroid.	
DR	Pfam; PF00104; hormone_rec; 1.	
DR	Pfam; PF00105; zf-C4; 1.	
DR	Pfam; PF02161; Prog_receptor; 1.	
DR	PRINTS; PR00047; STROIDFINGER.	
DR	ProDom; PD000035; znf_C4steroid; 1.	
DR	SMART; SM00430; HOL1; 1.	
DR	SMART; SM00399; znf_C4; 1.	
DR	PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.	
KW	Receptor; Transcription regulation; Nuclear protein;	
KW	zinc-finger; Steroid-binding.	
FT	DOMAIN 1 556 MODULATING, PRO-RICH.	
FT	DNA_BIND 557 622 NUCLEAR RECEPTOR-TYPE.	
FT	ZN_FING 557 577 C4-TYPE.	
FT	ZN_FING 593 617	
FT	DOMAIN 671 923 STEROID-BINDING.	
FT	DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).	
FT	SEQUENCE 932 AA; 99407 MW; 05384B9656BF22DC CRC64;	

QY 389 LHFSRMHATFSAWSL-----PGLQDTLVPPVTVTSQWVRSDV 428
 Db 505 MPHGG-PHSSFTYANMLPAMLCCKMGFAVLLVNYRGSTGFGQDSILSLPGNVGHQDVXD 563
 QY 429 QPAWKHL 436
 Db 564 QPAVEQVL 571

RESULT 11
 JAG2_RAT
 ID JAG2_RAT STANDARD: PRT; 1202 AA.
 AC P97607;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Jagged 2 (Jagged) (fragment).
 GN JAG2.

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97103852; PubMed=8948600;
 RA Shawber C., Boulter J., Lindsell C.E., Weinmaster G.;
 RT "Jagged2: a serrate-like gene expressed during rat embryogenesis.";
 RL Dev. Biol. 180:370-376(1996).
 CC -|- FUNCTION: PUTATIVE NOTCH LIGAND INVOLVED IN THE PERIPHERAL
 CC SIGNALING. MAY HAVE A ROLE IN NEUROGENESIS IN THE PERIPHERAL
 CC NERVOUS SYSTEM, LIMB DEVELOPMENT AND IN THE ADULT BRAIN.
 CC -|- SURCELLULAR LOCATION: Type I membrane protein.
 CC -|- DEVELOPMENTAL STAGE: AT STAGE E12.5 IT IS DETECTED IN DORSAL ROOT
 CC GANGLIA, AER, AND SURFACE ECTODERM. AT E14.5, FOUND AS WELL IN
 CC CRANIAL GANGLIA, THYMUS AND OLFACTORY EPITHELIA. AT E16.5, FOUND AS
 CC WELL IN SALIVARY GLAND, TOOTH BUDS AND HAIR FOLLICLES.
 CC -|- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
 CC -|- SIMILARITY: CONTAINS 1 DSL DOMAIN.

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 CC -----
 DR EMBL; U70050; AAC52946.1; -;
 DR HSSP; P00743; 1CCF.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001774; DSL.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_II.
 DR InterPro; IPR000083; Fibractnl.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF00008; EGF; 14.
 DR Pfam; PF01414; DSL; 1.
 DR PRINTS; PR00010; EGFBLD.
 DR PRINTS; PR00011; EGFAMININ.
 DR PRINTS; PR00012; FNTYPEI.
 DR SMART; SM00051; DSL; 1.
 DR SMART; SM00179; EGF_Ca; 7.
 DR SMART; SM00001; EGF_like; 8.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_10.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_15.
 DR PROSITE; PS01186; EGF_2; 11.
 DR PROSITE; PS01187; EGF_CA; 7.

Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
 Repeat: Transmembrane.
 KW NON_TER 1
 KW DOMAIN <1 1085
 FT TRANSMEM 1086 1102 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1103 1202 POTENTIAL.
 FT DOMAIN 132 194 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 195 228 DSL.
 FT DOMAIN 229 259 EGF-LIKE 1.
 FT DOMAIN 261 299 EGF-LIKE 2.
 FT DOMAIN 301 337 EGF-LIKE 3.
 FT DOMAIN 339 375 EGF-LIKE 4.
 FT DOMAIN 377 413 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 415 450 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 452 488 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 490 527 EGF-LIKE 8.
 FT DOMAIN 529 589 EGF-LIKE 9.
 FT DOMAIN 591 627 EGF-LIKE 10 (ATYPICAL).
 FT DOMAIN 629 665 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 667 703 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 706 742 EGF-LIKE 13.
 FT DOMAIN 744 780 EGF-LIKE 14.
 FT DOMAIN 782 818 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 819 880 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 199 210 BY SIMILARITY.
 FT DISULFID 203 216 BY SIMILARITY.
 FT DISULFID 218 227 BY SIMILARITY.
 FT DISULFID 230 241 BY SIMILARITY.
 FT DISULFID 236 247 BY SIMILARITY.
 FT DISULFID 249 258 BY SIMILARITY.
 FT DISULFID 265 277 BY SIMILARITY.
 FT DISULFID 271 287 BY SIMILARITY.
 FT DISULFID 289 298 BY SIMILARITY.
 FT DISULFID 305 316 BY SIMILARITY.
 FT DISULFID 310 325 BY SIMILARITY.
 FT DISULFID 327 336 BY SIMILARITY.
 FT DISULFID 343 354 BY SIMILARITY.
 FT DISULFID 348 363 BY SIMILARITY.
 FT DISULFID 365 374 BY SIMILARITY.
 FT DISULFID 381 392 BY SIMILARITY.
 FT DISULFID 386 401 BY SIMILARITY.
 FT DISULFID 403 412 BY SIMILARITY.
 FT DISULFID 419 429 BY SIMILARITY.
 FT DISULFID 423 438 BY SIMILARITY.
 FT DISULFID 440 449 BY SIMILARITY.
 FT DISULFID 456 467 BY SIMILARITY.
 FT DISULFID 461 476 BY SIMILARITY.
 FT DISULFID 478 487 BY SIMILARITY.
 FT DISULFID 495 506 BY SIMILARITY.
 FT DISULFID 500 515 BY SIMILARITY.
 FT DISULFID 517 526 BY SIMILARITY.
 FT DISULFID 544 567 POTENTIAL.
 FT DISULFID 561 577 POTENTIAL.
 FT DISULFID 579 588 BY SIMILARITY.
 FT DISULFID 595 606 BY SIMILARITY.
 FT DISULFID 600 615 BY SIMILARITY.
 FT DISULFID 617 626 BY SIMILARITY.
 FT DISULFID 633 644 BY SIMILARITY.
 FT DISULFID 638 653 BY SIMILARITY.
 FT DISULFID 655 664 BY SIMILARITY.
 FT DISULFID 671 682 BY SIMILARITY.
 FT DISULFID 676 691 BY SIMILARITY.
 FT DISULFID 693 702 BY SIMILARITY.
 FT DISULFID 710 721 BY SIMILARITY.
 FT DISULFID 715 730 BY SIMILARITY.
 FT DISULFID 732 741 BY SIMILARITY.
 FT DISULFID 748 759 BY SIMILARITY.
 FT DISULFID 753 768 BY SIMILARITY.
 FT DISULFID 770 779 BY SIMILARITY.
 FT DISULFID 786 797 BY SIMILARITY.
 FT DISULFID 791 806 BY SIMILARITY.
 FT DISULFID 808 817 BY SIMILARITY.
 SQ SEQUENCE 1202 AA; 129703 MW; 08CB44E5271FF8BE CRC64;


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RESULT 13
PRGR_RABIT STANDARD; PRT; 930 AA.
P06186;
AC AC
DT DT 01-JAN-1988 (Rel. 06, Created)
DT DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DE Progesterone receptor (PR).
GN GN PR OR NR3C3.
OS OS Oryctolagus cuniculus (Rabbit).
OC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
[1]
SEQUENCE FROM N.A.
MEDLINE=87067449; PubMed=3538016;
Loosfelt H., Atger M., Mistrahi M., Guiochon-Mantel A., Meriel C.,
Logeat F., Benarous R., Milgrom E.;
"Cloning and sequence analysis of rabbit progesterone-receptor complementary DNA."; Proc. Natl. Acad. Sci. U.S.A. 83:9045-9049(1986).
CC -! FUNCTION: THE STEROID HORMONES AND THEIR RECEPTORS ARE INVOLVED IN THE REGULATION OF EUKARYOTIC GENE EXPRESSION AND AFFECT CELLULAR PROLIFERATION AND DIFFERENTIATION IN TARGET TISSUES.
CC -! SUBCELLULAR LOCATION: Nuclear.
CC -! DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -! SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
NR3 SUBFAMILY.
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EMBL; M14547; AAA31443.1; -.
PIR; A25923; A25923.
HSP; P06401; 1A28.
TRANSFAC; T00697; -.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR000128; Progest_receptor.
InterPro; IPR001628; Znfc_C4steroid.
Pfam; PF001104; hormone_rec; 1.
Pfam; PF001105; zf-C4; 1.
Pfam; PF02161; Prog_receptor; 1.
PRINTS; PR00047; STROIDEFINGER.
ProDom; PD000035; Znfc_C4steroid; 1.
SMART; SM00430; HOLI; 1.
SMART; SM00399; Znf_C4; 1.
PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding.
DOMAIN 1 S65 MODULATING, PRO-RICH.
DNA_BIND 568 633 NUCLEAR RECEPTOR-TYPE.
ZN_FING 568 588 C4-TYPE.
ZN_FING 604 628 C4-TYPE.
DOMAIN 678 930 STEROID-BINDING.
DOMAIN 184 188 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SEQUENCE 930 AA; 98666 MW; 644FF4C13BF2F8B3 CRC64;
Query Match 2.9%; Score 102; DB 1; Length 930;
Best Local Similarity 20.1%; Pred. No. 5;
Matches 90; Conservative 49; Mismatches 160; Indels 148; Gaps 21;
QY 51 LAAPGPGSPQSGLGVCESTVPAVCASICCQAQVNFGASSTSWCNPKSLPHSSSIGDT 110
||||| |||| : | : | |||
db 418 LAAPPPLPPUPPSRRPGEAAVAAS-----PGSAVS-----SSSSSGST 458
```


Db 308 PSTPPEPE---VIPOVSLVPTLALLGLPIPRGNIQEVMAELFSGCEDSQPHSSALQA 364
 QY 376 WNVSMOTQAQQLLHFS-----RWHATESAA-----WSLPGLDQTLVPPY 418
 Db 365 SALHNAQVSRFLHYSAAATODLQAKELHQNLFSKASADYQWLLQSPRAEATLPTVI 424
 QY 419 TVSQVMSDVQF-AMKHLPCDVSRYHGLILIALALLTLLGVVLALTCRRPQSGP-P 476
 Db 425 AELQ-----QFLRGARACIE-SWARSILVRMAGTALLAASCFICLLASQWATSPGPF 477
 QY 477 ARPVLHRAADSQAQRLVGAELRAALGGROVVDLWGRHVARVGP-LPWLWAAR 535
 Db 478 FCLLLTPVAMG-----LVGAIA---YAGLLGTIELKLDLVILGAVAAVSSELPFLWKA- 528
 QY 536 TRVAREQGTVLLWSG-ADLRPVSGDPRAAPLALL-----HAAPRPLL 579
 Db 529 -----WAGWGSKRPLATLFPPIPGVLLLLRLAVFSDSVVAEARATPFL 575
 QY 580 LLAYFSLRCA-----KGDIPPLRALPRYRLRLDPLRLRALDARPAEATSWG-RLGARQ 634
 Db 576 LGSFILLVVLHWEQQLPP-----KLLTMRPLGTSATNPPRHNGAVALRLGI-- 625
 QY 635 RROSRLCSRL 646
 Db 626 ----GLLCTRL 633

RESULT 15

ID FHUB_SALTY STANDARD; PRT; 685 AA.
 AC 087656;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ferrichrome transport system permease protein fhbB (Ferrichrome uptake protein fhbB).
 GN FHUB OR STM0194.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
 RA "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2."
 RT Nature 413:852-856(2001).
 RL [2]
 RN SEQUENCE OF 467-685 FROM N.A.
 RC STRAIN-ATCC 14028S;
 RA Emmerth M., Goebel W., Miller S.I., Hueck C.J.;
 RT "Genomic subtraction identifies Salmonella typhimurium prophages and a novel fimbrial operon, stf, which are absent from S. typhi and E. coli."
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RL -!- FUNCTION: THIS IS ONE OF THE PROTEINS INVOLVED IN THE HIGH-AFFINITY TRANSPORT OF IRON(III)-FERRICHROME INTO THE E. COLI CELL.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM PERMEASE FAMILY. FECCD SUBFAMILY.

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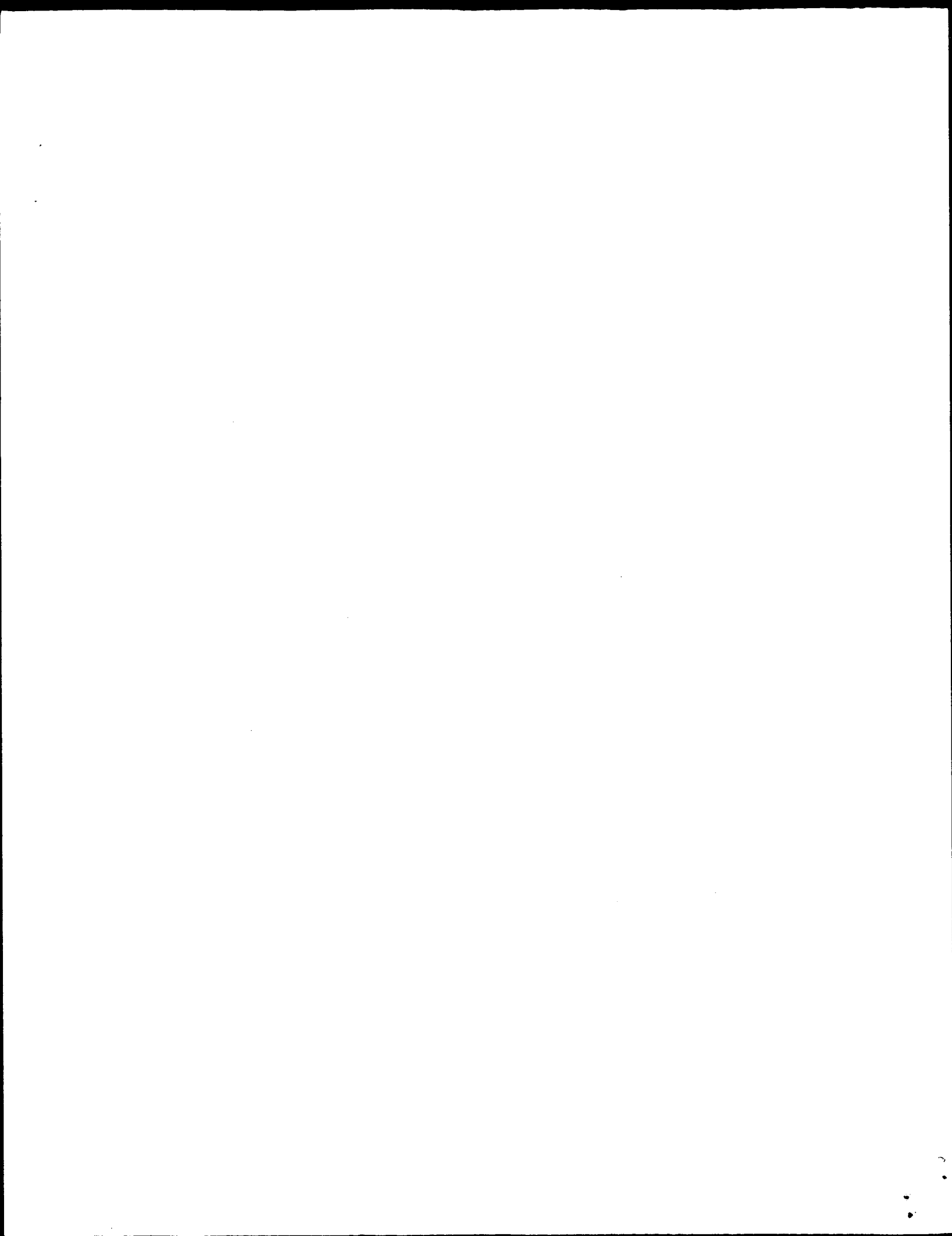
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AE008703; AAL19158.1; -
 CC EMBL; AF093503; AAC64151.1; -
 DR StyGene; SG10641; fhbB.
 DR InterPro; IPR000515; BPD.transp.
 DR InterPro; IPR000522; FecCD.
 DR Pfam; PF01032; FecCD; 1.
 DR PRODOM; PD001557; FecCD; 1.
 DR PROSITE; PS00402; BPD_TRANS_PNN_MBR; FALSE_NEG.
 KW Transport; Iron transport; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 35 55 POTENTIAL.
 FT TRANSMEM 88 108 POTENTIAL.
 FT TRANSMEM 120 140 POTENTIAL.
 FT TRANSMEM 143 163 POTENTIAL.
 FT TRANSMEM 172 192 POTENTIAL.
 FT TRANSMEM 266 286 POTENTIAL.
 FT TRANSMEM 302 322 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 373 393 POTENTIAL.
 FT TRANSMEM 416 436 POTENTIAL.
 FT TRANSMEM 456 476 POTENTIAL.
 FT TRANSMEM 479 499 POTENTIAL.
 FT TRANSMEM 504 524 POTENTIAL.
 FT TRANSMEM 553 573 POTENTIAL.
 FT TRANSMEM 592 612 POTENTIAL.
 FT TRANSMEM 632 652 POTENTIAL.
 FT TRANSMEM 660 680 POTENTIAL.
 FT CONFLICT 470 479 NAFGWLTPAG -> KPSGWYCLAE (IN REF. 2).
 FT CONFLICT 484 487 AAVL -> RRHW (IN REF. 2).
 FT CONFLICT 531 532 AE -> PK (IN REF. 2).
 SQ SEQUENCE 685 AA; 73203 MW; 547C0ACC551B353D CRC64;

Query Match 2.9%; Score 100.5; DB 1; Length 685;
 Best Local Similarity 22.2%; Pred. No. 4.5;
 Matches 93; Conservative 38; Mismatches 117; Indels 171; Gaps 19;

QY 345 HPQL-----CFKQVPWFSGNSHVECPHQTGSLTSWNVSMOTQAQQLLHFS----- 392
 Db 33 HPALLLLALFVAACWLTWNFS-VALPRSQWQAIAWSPDIDI-TEOMIFHYSQLPRLAIS 90
 QY 393 -----SRMHATESAANSLPG----- 407
 Db 91 LLVGAGLGLGVLFQOVLNRNLAEPPTLGVATGAQGLQITVTLWAIFGALTTPQAALTGA 150
 QY 408 -----LGQDT-----LVPPVY-----TVSQ 422
 Db 151 CIVGALVFGVAMGRKRLSPVTLILAGLVVSLYCGAINQLLVIFHHDQLQSMFLWSTGTLTQ 210
 QY 423 VWRSDVQFAWKHL-----CPDVSYRHLGL-LILALLLTLGLVLA 464
 Db 211 TDWSGVRLMPQLLGGVMLTLLLRPMTLMGLDDGVARNGLALSARLAALSIVLSA 270
 QY 465 LTCRRPQSGPGPARPVLILLHAADSEARRLVGA---LAELLRAALGGG-----RDVLDL 516
 Db 271 LLVN-----AVGIGFGLFAPLAKMLGARRLRLARLMAPLIGALILWLSDQII-L 321
 QY 517 WGRHVARVGPLPWLWAARTVAREQGTVLLLSGADLRPVSGPDPRAAPLAA----- 569
 Db 322 W-----LTRV-----WNEVSTGVTALIGAPLLLLPRLKMSAPDMNASDRVAERHVL 373
 QY 570 LLHAAPRPLLALVFSRLC-----AKGDIPPLRALPRYRLRLDPLRLRALDA 618
 Db 374 AFVAGGALLLTLATWVALSFGDRAGHTWASGTL---LEELMPWR-----WPRILAALMA 425

Search completed: January 28, 2003, 09:29:42
 Job time : 22 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 28, 2003, 09:28:03 : Search time 37 Seconds
(without alignments)
3658.729 Million cell updates/sec

Title: US-09-863-818A-12
Perfect score: 3512
Sequence: 1 MGSSRLAALLPLLLIVIDL.....SRLELCRLREARLADLG 657

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL.21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertebrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1521.5	43.3	482	Q8TEC2	Q8tec2 homo sapien
2	1023	29.1	311	Q8R335	Q8r335 mus musculus
3	163.5	4.7	538	Q9BR97	Q9br97 homo sapien
4	159.5	4.5	567	Q99J43	Q99j43 mus musculus
5	122.5	3.5	474	Q73906	Q73906 gallus gall
6	113.5	3.2	1199	Q8W29	Q8w29 homo sapien
7	113.5	3.2	2864	Q59422	Q59422 hepatitis g
8	111.5	3.2	515	Q9RRK1	Q9rrk1 deinococcus
9	110.5	3.1	381	Q63095	Q63095 rattus norv
10	107	3.0	558	Q8KY53	Q8ky53 streptomyce
11	106.5	3.0	4268	Q8XYF2	Q8xyf2 ralsstonia s
12	106	3.0	428	Q88003	Q88003 bordetella
13	106	3.0	1463	Q70320	Q70320 cavia porce
14	105.5	3.0	7576	Q9ZGA4	Q9zga4 streptomyce
15	105	3.0	523	Q9HW81	Q9hw81 pseudomonas
16	105	3.0	587	Q8R0M9	Q8r0m9 mus musculus

17	105	3.0	2864	12	Q999T0	Q999t0 hepatitis g
18	104.5	3.0	847	11	Q9J564	Q9jj64 mus musculus
19	104	3.0	709	16	Q9RYK7	Q9ryk7 deinococcus
20	104	3.0	732	6	Q9TS46	Q9ts46 sus scrofa
21	103.5	2.9	401	16	Q9S221	Q9s221 streptomyce
22	103.5	2.9	498	16	Q9KXK2	Q9kxk2 streptomyce
23	102.5	2.9	606	16	Q9KY63	Q9ky63 streptomyce
24	102.5	2.9	1034	11	Q35888	Q35888 rattus norv
25	102.5	2.9	1456	2	Q9F636	Q9f636 stigmatella
26	102.5	2.9	2358	16	Q9LIV8	Q9lliv8 streptomyce
27	102	2.9	253	4	Q8W2B4	Q8wzb4 homo sapien
28	102	2.9	396	16	Q9EWX4	Q9ewx4 streptomyce
29	102	2.9	576	4	Q9Y2X4	Q9y2x4 homo sapien
30	102	2.9	576	4	Q9BRG2	Q9brg2 homo sapien
31	102	2.9	829	10	Q9SYA0	Q9sya0 arabidopsis
32	102	2.9	2035	16	Q8ZF24	Q8zf24 yersinia pe
33	102	2.9	2041	2	Q9Z399	Q9z399 yersinia pe
34	101.5	2.9	513	2	Q8VPV8	Q8vpv8 synechococc
35	101.5	2.9	690	16	Q9L0N2	Q9l0n2 streptomyce
36	101.5	2.9	6315	2	Q9ADL6	Q9adl6 polyangium
37	101	2.9	428	2	Q45374	Q45374 bordetella
38	101	2.9	482	16	Q9I4A0	Q9i4a0 pseudomonas
39	101	2.9	906	16	Q9HX92	Q9hx92 pseudomonas
40	101	2.9	4809	2	Q33HH0	Q33hh0 streptomyce
41	100.5	2.9	392	4	Q9NT84	Q9nt84 homo sapien
42	100.5	2.9	1438	16	Q85739	Q85739 pseudomonas
43	100	2.8	1193	2	Q9Z5E0	Q9z5e0 rhodobacter
44	100	2.8	2864	12	Q9QEW5	Q9qew5 hepatitis g
45	99.5	2.8	1101	11	Q9JJI6	Q9jjj6 mus musculus

ALIGNMENTS

RESULT 1

Q8TEC2
ID Q8TEC2 PRELIMINARY; PRT; 482 AA.
AC Q8TEC2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CDNA FLJ23658 fis, clone COLF3416.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON MUCOSA;
RA Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074238; BAB85028.1; ..
SQ SEQUENCE 482 AA; 54139 MW; 4164B5A73026B385 CRC64;

Query Match	43.3%	Score	1521.5;	DB 4;	Length	482;			
Best Local Similarity	69.7%;	Pred. No.	7.3e-113;						
Matches	313;	Conservative	15;	Mismatches	54;	Indels	67;	Gaps	10;
QY	1	MGSSRLAALLPLLLIVIDLSDSAGIGRFRHLPHWNTRCPPLASHTEVLPISLAAPGGPSSP	60						
Db	1	MGSSRLAALLPLLLIVIDLSDSAGIGRFRHLPHWNTRCPPLASHTD	45						
QY	61	QSLGVCSGTVPAVCASICCCQVAQVFNCGASSTSCRNPKSLPHSSSIGDTRCOHLL	116						
Db	46	-----DSFTGSSAYIPCRITWAL--FSTRPWC---VRVWCHSR---CICQHLSSGS	89						
QY	117	---RGSCCLVTCRLRAITF-----PSPQTS--PTRDFALKGNLRIQRHGKVPFD	163						
Db	90	GLQRLHLLVQKSKSSTFFRYRHKMPAPQAQRLLPRLHSEKSHHISIPS	144						

QY 164 WTHKGM-----EVGTGNNRWVQLSGGPEFSDLLPEARAIRVTISSGPEVSRL 213
 Db 145 ISHGLRSKRTQSPDETWSLPRLDSSRGHGPEFSDLLPEARAIRVTISSGPEVSRL 204
 QY 214 CHOWALECELSPPYDQKIVSGGHTVPELPLCLICIEASYLQEDTVRRKKCPFQSW 273
 Db 205 CHOWALECELSPPYDQKIVSGGHTVPELPLCLICIEASYLQEDTVRRKKCPFQSW 264
 QY 274 PEAYGSDFWKSVHFTDYSOHTQWVWALTURCPKLEAALCORHWHITCKDLPLNATARES 333
 Db 265 PEAYGSDFWKSVHFTDYSOHTQWVWALTURCPKLEAALCORHWHITCKDLPLNATARES 324
 QY 334 DGWYLVLEKVDLHPQLCFKVPWFSGNSHVECPHOTGSLTSWNVSMDTQAQOILHFFSS 393
 Db 325 DGWYLVLEKVDLHPQLCFK----FSGNSHVECPHOTGSLTSWNVSMDTQAQOILHFFSS 380
 QY 394 RMHATSAWSLPLGLQDPLVPPVTVSQ 422
 Db 381 RMHATSAWSLPLGLQDPLVPPVTVSQ 409

RESULT 2

Q8R335 PRELIMINARY; PRT; 311 AA.
 AC Q8R335;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 34.1 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026737; AAH26737.1;
 KW Hypothetical protein.
 SQ SEQUENCE 311 AA; 34102 MW; 00E706D6617CFF15 CRC64;

Query Match 29.1%; Score 1023; DB 11; Length 311;
 Best Local Similarity 71.3%; Pred. No. 2e-73;
 Matches 211; Conservative 17; Mismatches 44; Indels 24; Gaps 2;

QY 380 MDQAQOILHFFSSRMHATFSAWSLPLGLQDPLVPPVTVSQ-----422
 Db 1 MDQAQOILHFFSSRYATFSAWSLPLGLQDPLVPPVTVSQ-----422
 QY 423 -----VRSDFQFAWKHLCPDVSRYRHGLLILALLLTLGLVVALTCRRPQSGPP 476
 Db 61 QENCILVRSDFQFAWKHLCPDVSRYRHGLLILALLLTLGLVVALTCRRPQSGPP 476
 QY 477 ARPVILLHAADSEARRLVGAELLRALGGROVIVDLWEGRHVARVGPLPWLWAART 536
 Db 121 TRPVLLHAADSEARRLVGAELLRALGGROVIVDLWEGRHVARVGPLPWLWAART 180
 QY 537 RVAREQGVLLWGSADLRVSPGDPRAAPLALLHAAPRPLLLAYFSRLCAKGDIPPP 596
 Db 181 RVAREQGVLLWGSADLRVSPGDPRAAPLALLHAAPRPLLLAYFSRLCAKGDIPPP 239
 QY 597 RLALPYRLRLDLPLRLALDAPFAEATSWGRLGARQRQRSLRLEAREAR 652
 Db 240 RLALPYRLRLDLPLRLALDAPFAEATSWGRLGARQRQRSLRLEAREAR 295

RESULT 3

Q9BR97 PRELIMINARY; PRT; 538 AA.
 AC Q9BR97;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE Hypothetical 59.1 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC006411; AAH06411.1;
 KW Hypothetical protein.
 SQ SEQUENCE 538 AA; 59127 MW; 65E6344DA6A5AFD2 CRC64;

Query Match 4.7%; Score 163.5; DB 4; Length 538;
 Best Local Similarity 22.7%; Pred. No. 0.0001;
 Matches 128; Conservative 56; Mismatches 184; Indels 197; Gaps 32;

QY 36 TRCPPLASHTVLPISLAAPGGSPSQSL-----GVCESGTPAVCACTCCQVAVFGASS 91
 Db 78 TDCDLCLR---VAVRLAVHGHWEPEDEKFGGAADSGVEPRNASLQAQVLSFQ-AYP 133
 QY 92 TSWC-----RNPKSL-PHSSSIGDTRCOHLLRGSCCLVVTCLRRATFPSPQTSPTDF 145
 Db 134 TARCVLLEVOVPAALVOFGQSVGS-----VYDCFEAAL-----GSEVRIM 174
 QY 146 ALKGPNLRIQ-RHGKVPF-----DWTHKGMVGT-----GYNNRWVQLSGGPEFS 189
 Db 175 SYTOPRYEKELNHTQQLPALPWLNVADGNVHLVNLVSEEQHGLSLYWNQVQPK-- 232
 QY 190 FDLLEPRAIRIVTISGPEVSVRICHOWALBCEBLSPPYDQKIVSGGHTVPELPL 249
 Db 233 -----PRW-----HKNLTGPQITLNLHTDLVP 254
 QY 250 CLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYSOHTQWVWALTUR 303
 Db 255 CLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSVHFTDYSOHTQWVWALTUR 303
 QY 304 -CPKLEAALCORHWHITCKDL-----PNATARESDFWVLEKVDL--HPQLCFKVP 354
 Db 304 PCSLPAEALCORHWHITCKDL-----PNATARESDFWVLEKVDL--HPQLCFKVP 356
 QY 355 WFSFGNSH-----VEC--PHOTGSLTSWNVSMDTQAQOILHFFSSRMHATF--SAWSL 406
 Db 357 -----NSSEKLQLOECLWADSLGPLKDDVLLLETRGPQ-----DNRSICALEPSCGTS 406
 QY 407 G-----LGQDILVPPVTVS-----QVWRSDFQFAWKHLCPDVSRYRHGLLIL 450
 Db 407 SKASTRAARLGE-----YLLQDLQSGQCLQDWDLLGALW---ACPMKYIHKRWALV 456
 QY 451 ALLALLTLGLVVALTCRRPQSGPPARPVILLHAADSEARRLVGAELLR-----504
 Db 457 WLACL--LFAAALS-----ILLKKDHAKGWRL--LKQDVRSGGEWEQ 497
 QY 505 ALGGRDVIVDLWEGRHVARVGPLP 529
 Db 498 ALGGGPP-----PCSQACASSPLP 516

RESULT 4

Q99J43 PRELIMINARY; PRT; 567 AA.
 AC Q99J43;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 62.8 kDa protein.
 GN ILI/RL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004759; AAH04759.1; -
DR MGI; MGI:2159336; I117rl.
KW Hypothetical protein.
SQ SEQUENCE 567 AA; 62798 MW; CIAAAB79E2006BID CRC64;

Query Match 4.5%; Score 159.5; DB 11; Length 567;
Best Local Similarity 21.3%; Pred. No. 0.00023;
Matches 111; Conservative 65; Mismatches 217; Indels 127; Gaps 23;

QY 32 PHWTRCPLASHTV-----LPISL-AAAGGSSPSQSLGV-----CEGTVPVAVCASI 78
Db 27 PODTARCSLGLSCHLWDGVLCPGLSLOSAPGVLVPLRLQTELVLRCPOKTDALCVRV 86
QY 79 CCQVAQVNGASTSWCRNPKSLPHSSSIGDTRCQHLRGSCCLVVTCLRRRAITFPS--- 135
Db 87 VVHLAVGHVHABPEEAGKSDSELSERN-ASLQAQWLSFQAYPIARCALLEVOVPADLV 145
QY 136 -PQOTSPTDF---ALGPNLRIORHGK-----VFPDTHKGMVGTGYNRRW 179
Db 146 PQQSVGSAVDFCFEASLGAEOIWSYTKPRYQKELNLTQQLPDC--RGLEVRDSIQSCW 203
QY 180 V-----QLSGGPEFSFDL-----LPEARAIRVTISSGPEVSVRLCHOWA 218
Db 204 VLPWLVNSTDGDVNLVLLTLDVSEQDFSELLYLRPVDA-----LKSLLW- 246
QY 219 LCEBELSPYDQKTVSGGHTVELPYELLPCLCIEASYLQEDTVRRKKCPQSWPEAYG 278
Db 247 -----YKNLTGQPNITLNTDLVPCLCIQVNSLEPDSERVEFCFPREDPGAH- 293
QY 279 SDFWKSVMHTDYDQHTQVMWMLTLCPLKLEALCQRHWDHTLCKDL-----PNATARE 332
Db 294 RNLW---HJARVLSPGVWQMDAPCCLPKVTLCWQAPDQSPQCPPLVPPVQKNATVNE 350
QY 333 SDGWTVLEKVDLHPOLCFKVPWFSGNSHVECPHQTSGLTSWNVSMDTQAQQLILHFS 392
Db 351 PDFE---QLVAGHPNLQVQSTW---EKVQLACLWADSLGPFKDDM-----LLVEMK 397
QY 393 SRMHATF-----SAANSLPG-----LGQDTLVP-PVYTVSVWRSQ-VQFAWKHL 436
Db 398 TGLNNTSVCALEPSCGCTPLPSMASTRARLGBELLQDFSRHQCMLWDDNNGSLW---A 454
QY 437 CPDVSYRHGLLILALLLTLGLVVLATCRPPQSGP 476
Db 455 CPMDYIHRWVVLWVLAALLAAALFFLLKKDRMTSP 494

RESULT 5
O73906
ID O73906 PRELIMINARY; PRT; 474 AA.
AC O73906;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE CD5 protein precursor.
GN CD5
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H.B2; TISSUE=THYMUS;
RX MEDLINE=98250124; PubMed=9590242;
RA Koskinen R., Goebel T.W.F., Tregaskes C.A., Young J.R., Vainio O.;
RT "The structure of avian CD5 implies a conserved function."
RL J. Immunol. 160:4943-4950(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B12;

RX MEDLINE=21332904; PubMed=11439160;
RA Koskinen R., Salomonsen J., Goodchild M., Bumstead N., Boyd Y.,
RA Vainio O.;
RT "Structure and chromosomal localization of chicken CD5."
RL Scand. J. Immunol. 54:141-145(2001).
DR EMBL; Y12011; CAA72739.1; -
DR EMBL; AJ306429; CAC43844.1; -
DR InterPro; IPR011190; Srcr_receptor.
DR Pfam; PF00530; SRCR; 3.
DR SMART; SM0202; SR; 3.
DR PROSITE; PS0287; SRCR_2; 3.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL
SQ SEQUENCE 474 AA; 50998 MW; 3AF2BB41591AE0E6 CRC64;

Query Match 3.5%; Score 122.5; DB 13; Length 474;
Best Local Similarity 20.9%; Pred. No. 0.16;
Matches 110; Conservative 52; Mismatches 190; Indels 175; Gaps 24;

QY 12 PLLIVIDLSDSAGIGFR-----HLPWNTRCPLASHTVLPISLAAPGPPSP 60
Db 6 PALCLLVGMWAGCGGAVLGAAGAAKPLRLSGGCR-----AGLEVOQMSSRWS- 57
QY 61 QSLGVCESGTVP-AVCASICQVAQVFNGA-----SSTSWCRNPKSLPHSSSIGDTRCOH 114
Db 58 ----VWDGVSFGVSGVQLGCRPPAKLSSAPPDLLEQQAWAMOCK-----GMERCQ- 104
QY 115 LLRSGC---LVVTCLRRRAITFPSPQTSPTDRFALKPNLRIORHGKVPDPWTHKMEV 171
Db 105 -WKAANCQHAQVAVTCSPEPTSTKPPSPPTTS-----PEPT----- 140
QY 172 GTGYNRWVQLSGGPEFSFDLLPEAR-----AIRVTISSGPEVSVRLCHOWALECELS 225
Db 141 ----GAPWLRVLDG-NFSCSGFVELHLRGMGAVALSVDWVPELPARICRE--LGC--N 190
QY 226 SPYDVQIVSGGHVPELPEFLPCLCIEASYLQEDTVRRKKCPQSWPEAYGSDFWKSV 285
Db 191 NPSGVPMGPGMGPVSLPQSRLP-----VRWEAVAPCSSPELLCCFNWTS- 236
QY 286 HFTDYSOHTOMVMALTLRCPKLEAA-----LCQRHWDHTLCKDLPNAT 329
Db 237 -----HGHKASAFILCPGSPRAGRRLAGGTPCEGHIEVFQRGOWHTLCEQAH-- 287
QY 330 ARESGHWVLEKVDLHPOLCFKVPWFSGNSHVECPHQTSGLTSWNVSMDTQAQQLIL 389
Db 288 -----RVERGHQLCRELR-CGDLSSEAELQEPFRAGGVICKERYLHLCPESP 335
QY 390 HFSSRMHATFSAWSLPLGLQDTLVPPVTVYSQVWRSQVFAWKHLCPDVSYRHGLLI 449
Db 336 HGCSRTHV-----VCQKSKPPAGTAP-----GTVA 361
QY 450 LALLALTLGVVLATCRPPQSGPAPRVLLHAAADSEAQRRLVG 496
Db 362 SICLALL-LLGVLL-LIC-----GPPAVRRLMKRISKKKQKQWIG 399

RESULT 6
O8WW29
ID O8WW29 PRELIMINARY; PRT; 1199 AA.
AC O8WW29;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Hypothetical 133.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

Nature 417:141-147(2002).

EMBL; AL356832; CAB92674.1; -.

SQ SEQUENCE 558 AA; 55368 MW; 38A2BC41EF030EE7 CRC64;

Query Match 3.0%; Score 107; DB 16; Length 558;

Best Local Similarity 26.3%; Pred. No. 3.3;

Matches 74; Conservative 28; Mismatches 93; Indels 86; Gaps 13;

QY 405 LPGLGQDPLVP-PVYTVSQVWRSVQFAWKHLLCPDVSYSRHGLGLLILALLALLLLGW- 462

DB 1 MAGVLTQTTARFAPLSLLTRWD-----RSPGLAAGLLGGVAAVLGAACAALVT 51

QY 463 -LALTCRRPQSGPGFAPRVLLHHAADSAQRRLVGAELRAALGGGRDVIIDLWEGRH 521

DB 52 LLIWISSPYDSGPGA-----LHVA---AALWVLAHGAELVRADTLSTGP----- 93

QY 522 VARVGPLP-----WLWAARTVAREQGTVLLWSGADLRPVSGDDPRAAPLLALLHA 573

DB 94 -APVGVTPLELLPLPVLLHRAARDATDPDGGVGAVGA--APKAGPGARPANMASPDT 150

QY 574 APRPL-----LLAYFS-----RLCAKGD-----IPPLRAL----- 600

DB 151 GPPVSVARVANTGVVGLVAVGPVLLTAQGGALRPASAWAAVCLPLVAMGAAGAVWTA 210

QY 601 -----PRYLRDLRLLRALDARPAEATSWGRIGARQR 635

DB 211 FGRPGPGVGRALRVLPKRLMLVEPDA-----RLGAATR 245

RESULT 11

ID Q8XYF2 PRELIMINARY; PRT; 4268 AA.

AC Q8XYF2;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Probable polyketide synthase protein.

GN RSC1806 OR RS04228.

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;

OC Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GMI1000;

RX MEDLINE=21681879; PubMed=11823852;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Chandelier M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,

RA Siguier P., Thebaud P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:437-502(2002).

DR EMBL; AL646066; CADI508.1; -.

DR InterPro; IPR001227; Ac transferase.

DR InterPro; IPR000873; AMP-bind.

DR InterPro; IPR001242; Condensatn.

DR InterPro; IPR000794; Ketoacyl-synt.

DR InterPro; IPR001601; Methyltransf.

DR InterPro; IPR003880; Ppanne-attach.

DR InterPro; IPR000408; Reg_chir_condens.

DR InterPro; IPR000051; SAM_bind.

DR pfam; PF00698; Acyl trans; 1.

DR pfam; PF00501; AMP-binding; 2.

DR pfam; PF00668; Condensation; 2.

DR pfam; PF00109; ketoacyl-synt; 1.

DR pfam; PF02801; ketoacyl-synt_C; 1.

DR pfam; PF00550; pp-binding; 4.

DR PRINTS; PR00154; AMPBINDING.

DR PROSITE; PS00075; ACP_DOMAIN; 4.

DR PROSITE; PS00455; AMP_BINDING; 2.

DR PROSITE; PS00606; B_KETOACYL-SYNTHASE; UNKNOWN_1.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_2.

DR PROSITE; PS00626; RCC1_2; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 4268 AA; 457109 MW; 960E31222B7A30DF CRC64;

Query Match 3.0%; Score 106.5; DB 16; Length 4268;

Best Local Similarity 20.5%; Pred. No. 47;

Matches 98; Conservative 39; Mismatches 151; Indels 189; Gaps 21;

QY 305 PKLEAALCORHDHHTLCKDLPNATARESNGVYVLEKVDLHQLCFKVPWFSGNSSHV 364

DB 3751 PNGMQRVLPVPDYRIACODLRGCAAEVSEWLEIVRLE-----SH- 3792

QY 365 ECPHQTSLSWNV-----SMDTQAQOLI-----LHFSRMHATFSAAWSLPLGQDPL 413

DB 3793 EAPDTTG-----WPLFTVRAARMSDTRIRLIFSLDNLVCDGRSMRTLLAEWSRLAREPGTV 3848

QY 414 VPPV-----YTVS-QVWR-----SDVQFA 431

DB 3849 LPPLSATFRDYVLLTEQLALRPYSQSLRYWHDKLTLPAPALPRGRHAADAVSPHFT 3908

QY 432 WKHLLCPDVSYRHL-----GLLIALLALLTLLGVVLAITC-----RRPOS 472

DB 3909 RREASLPPAQMQALQRAAQAQGVTVNAL--LLAAYGEVLANWCATPRTINTLTFNRPV 3966

QY 473 GP-----GPAPRVLL-----HAADSEAQRRL-----VGALAEILLRAA--- 505

DB 3967 HPOIDALVGDFTSVLLAFDGTAAALGFAQALAMQOIWADLEHMQVSAVRVLEAARN 4026

QY 506 -----LGGGRDVIVDLWEGRHIVARGPLPWLWAARTVAREQGTVLL 548

DB 4027 RRLDPVAMPVVFVTSGLGVAGDGDSEMD-WLGHFVYGVVSTPQWIDQ-QVVERNGALVTN 4084

QY 549 WSGADL-----RPVSGPDPR-----AAPLLALLHAA 574

DB 4085 WDAVDTLFPDGLDDMFAYRDLRLRLAPOEAMQRPVGGDLPASWPVAAAPASAAQA 4144

QY 575 PR-----PLLLL-----AFSRLCARGDIPPPRALPRYRLRLDRLPRLRALDA 618

DB 4145 PQADAGPALAVDDAILATVRGMLGALTGRGELPVQVNFELGATSLDLRLRLQQLWA 4201

RESULT 12

O88003

ID O88003 PRELIMINARY; PRT; 428 AA.

AC O88003;

DT 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE Putative 3-deoxy-D-manno-octulosonic-acid transferase.

GN WAAA.

OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).

OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

OC Bordetella.

OX NCBI_TaxID=518;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CN7635E;

RX MEDLINE=99346157; PubMed=10417135;

RA Preston A., Allen A.G., Cadisch J., Thomas R., Stevens K.,

RA Churche C.M., Badcock K.L., Parkhill J., Barrrell B., Maskell D.J.;

RT "Genetic Basis for Lipopolysaccharide O-Antigen Biosynthesis in

RT Bordetella."

RL Infect. Immun. 67:3763-3767(1999).

DR EMBL; AJ007747; CAA07673.1; -.

DR InterPro; IPR001296; Glycos.transf_1.

DR Pfam; PF00534; Glycos.transf_1; 1.

KW Transferase.

SQ SEQUENCE 428 AA; 45386 MW; 9F3B59629D92D5E1 CRC64;

Query Match 3.0%; Score 106; DB 2; Length 428;

Best Local Similarity 24.6%; Pred. No. 2.9;

Matches 70; Conservative 22; Mismatches 91; Indels 102; Gaps 12;

QY 423 VMSDVQFAMKHLCLPDVSYRHL-----GLLILA-----LLALLTLGQVVLALTCRRP 470
 Db 103 IGRQLOQAMLPDYDFGATRRFLARHAPRCGLLIEREVNPLNLAARAQGV-----153
 QY 471 QSGGPARPVLLHHAADSEARRLVGAELRLAALGG-GRDIVDLMEGRHVARVGPLP 529
 Db 154 -----PMALVSAREFSASSLRQAGWLGOALREALAGLGRVLAQTDGARGLCQAGANA 205
 QY 530 W-----LWAATRVAREQGTVLLWSGADLRPV-----SGDDPRAAPLLALL 571
 Db 206 YTVTGSLLKFDVALPEAQLRVGH-----AWAGATGRPVIALASTREGEDAMFIEAIGAL 258
 QY 572 H-----AAPRLPLL-----LAFVRLCAKGDIPPLRALPRYRLLR 607
 Db 259 QAHRAATPRPLLILPRPHORFDEAQAQLOAGLAVARRSAGSGEGCPHIDVL-----311
 QY 608 DLPRLLRALDARPPAEAT-----SWGRLGARQRQRSLRLCS 644
 Db 312 ----LGDTLGEMPFFYAAADVAIVGGSFARLGG-----QNLEIACA 348
 RESULT 13
 ID 070320 PRELIMINARY; PRT; 1463 AA.
 AC 070320;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Phospholipase B.
 GN PLB.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CR1.(BFA)BR; TISSUE=INTESTINE;
 RX MEDLINE=98256256; PubMed=9593672;
 RA Delagebeaudet C., Gassama-Diagne A., Nauze M., Ragab A., Li R.Y.,
 Capdevielle J., Ferrara P., Fauvel J., Chap H.;
 RT "Ectopic Epididymal Expression of Guinea Pig Intestinal Phospholipase
 B. Possible role in sperm maturation and activation by limited
 proteolytic digestion.";
 RL J. Biol. Chem. 273:13407-13414(1998).
 DR EMBL: AF045454; AAC40129.1; --
 DR InterPro: IPR001087; Lipase_GDSL.
 DR InterPro: IPR003662; Sub.transporter.
 DR Pfam: PF00657; Lipase_GDSL; 3.
 DR PROSITE: PS01098; LIPASE_GDSL_SER; 2.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
 SQ SEQUENCE 1463 AA; 162175 MW; 101C4969819F24B1 CRC64;

Query Match 3.0%; Score 106; DB 11; Length 1463;
 Best Local Similarity 20.4%; Pred. No. 13;
 Matches 84; Conservative 46; Mismatches 136; Indels 146; Gaps 20;

QY 143 RDAFGKPNRIORHGKVPDPWTHKMEVGTGYNRRWVQLSGGPEFSLLPPEARIVT 202
 Db 444 REF-----NPSL-----KGFSTGTGKANSVGAFNNQAVAGARAG-----DLIPOARTLVLDL 489
 QY 203 ISSGPEVSVRLCHQWALECEELSSPYDVQKIVS---GGHVELPYEFLPLCLIEASYLQ 259
 Db 490 MKN---HTSINFEDW-----KLIITVFIGNDL-----514
 QY 260 EDTVRRKKCPQSQWPEAYGSDFWKSVHFTD-----YSQHTQVMVMTLIR 303
 Db 515 -----CDFCSDPVNTSP-----NFTDNIRQALDILHAEVPRAVNMVKVLIQVNL 561
 QY 304 -----CPLKEALCORHWHLCKDLPNATRESGWVYLEK-----341
 Db 562 ELYKDSRVSCPRILNLCR-----CVLLPDDNSTELESLLIDINKYQERTHQLIESG 614

QY 342 -VDLHPQLCFKVPWFSGNCSHVPCPHOTGSLTSMNVSMDFQAQQLILHFSRRMHA-TF 399
 Db 615 RYDTRDFTVVLPQPF-----EKVDIPK-----TSEGLPDNTSPAPDCFHFSSKTHAAA 664
 QY 400 SAANS--LPLGLQDILVPVTVSVQWRSDVQFAMKHLCLCPDVSYRHLGLLITALLALIT 457
 Db 665 SALWNKMLEPVQOK-----TQNNFENSID-----IICPNQAFPLYLSTYKNG-----706
 QY 458 LIGVVALTCRRPQSGPGPARPVLLHHAADSEARRLVGAELRLAALGG 509
 Db 707 IEHGHTWLTCTERTPSASPTSVHALRPADV-----RVVAALGDSLITAGSGIG 754
 RESULT 14
 ID Q9ZGA4 PRELIMINARY; PRT; 7576 AA.
 AC Q9ZGA4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE FK506 polyketide synthase.
 GN FKBB.
 OS Streptomyces sp. MA6548.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=82632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MA6548;
 RX MEDLINE=98451508; PubMed=9780228;
 RA Motamedi H., Shafiee A.;
 RT "The biosynthetic gene cluster for the macrolactone ring of the
 immunosuppressant FK506.";
 RL Eur. J. Biochem. 256:528-534(1998).
 DR EMBL: AF082100; AAC68815.1; --
 DR HSP: P08659; 1LC1.
 DR InterPro: IPR001227; AC.transferase.
 DR InterPro: IPR002085; Adh_zn_family.
 DR InterPro: IPR000873; AMP-bind.
 DR InterPro: IPR000292; For/Nit_trnsprt.
 DR InterPro: IPR001899; Gram_pos_anchor.
 DR InterPro: IPR000794; Ketoacyl-synt.
 DR InterPro: IPR003880; Peantne_attach.
 DR InterPro: IPR003862; sub.transporter.
 DR Pfam: PF00698; Acyl_transf; 4.
 DR Pfam: PF00107; adh_zinc; 1.
 DR Pfam: PF00501; AMP-binding; 1.
 DR Pfam: PF00109; ketoacyl-synt; 4.
 DR Pfam: PF02801; ketoacyl-synt_C; 4.
 DR Pfam: PF00550; pp-binding; 5.
 DR PROSITE: PS00075; ACP_DOMAIN; 5.
 DR PROSITE: PS00455; AMP_BINDING; 1.
 DR PROSITE: PS01005; FORMATE_NITRITE_TP_1; UNKNOWN_1.
 DR PROSITE: PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.
 DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_4.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 KW Phosphopantetheine; Transferase.
 SQ SEQUENCE 7576 AA; 790105 MW; 49765AB9E66DD96 CRC64;

Query Match 3.0%; Score 105.5; DB 2; Length 7576;
 Best Local Similarity 20.6%; Pred. No. 1.2e+02;
 Matches 140; Conservative 62; Mismatches 199; Indels 279; Gaps 35;

QY 16 IVIDLSDSAGIFRHLPHW-----NTRCPLASHP-----EVLPIISLAAPG 55
 Db 5190 VAVDPEVIGARPTDPLPHLPYFFERTYWLGSRAAGDAAPAGQLPVAHPVLTAAVMYPG 5249
 QY 56 -----GPSSPQSLGVCESGTVPAVCASICQVAVFGASSTSWCRNP-----KSL 101
 Db 5250 TGDVLVTGRVEATDPLATRVHPGAARAVLLDLRSRA---TKRAAAPRRSPWTPRSAL 5306
 QY 102 PHSSSIGDTRCOHLRLGSCCLVVTCL-----RRAITFPSPQTSPTDFALKGNLRIO 155

Db 5307 PQS -----GGALSVTVAAAGCGDGRRAVAVHARPGTG----- 5338
QY 156 RUGKVPFWTHKGMVGTGYNRWQSLGCGPESFDLLPEARAIRVTISSGPEVSVRLCH 215
Db 5339 -----EWT-----EHATGILARVARV-----ASAVPETSPWPPATAR----- 5371
QY 216 QWALECEELSSPYDV-----OKTVSGGHT-----VELPYEFLPCLCIEASYLQEDTVRRKKCP 269
Db 5372 -----PFDVGLADRLARAGHTDGPALPR----- 5396
QY 270 FOSWPEAYGDFWKSVEHFTDYSOHTQVMNALTLCPLKLEALCQRHDMHTLCKDLPNAT 329
Db 5397 RAAWAD-----DDAVHAEVALA-----DEQHAD 5419
QY 330 ARESDGWVLEKVDLHPQLCFKVPWFSEFGNSSHVECP-----HOTG-----SLTS 375
Db 5420 A-----ERYGLHPALLGAALALAGEG-----ADLPSAFDDVRVHATGATTVRVAVTA 5466
QY 376 WNVSMDOQAQQLILHFSSRMHATFSAANSLPGLGODTL-----VPPVTVTSQVWRSVDQF 430
Db 5467 TGIHLADETGPSVAIVGAVRRRPLVEGAVFGLLRPDIAETAELEPPT-TATGGGLDDP-- 5523
QY 431 AMKHLCPDV-----SYRHIGLILALL-ALLT-----LLGVVLALTCRRPQS 472
Db 5524 -----VPPDWILPAHGTGGGPGTETDGLGARVLAALRSFLTDDRYADAVLAV-----HT 5573
QY 473 GPG--PARPVLLHRAADSEAQRRLYCALAE-----LLRAALGGGRDVIQVWEGRHVAR 524
Db 5574 GPGLAAPAAAGLVRTQAQAEHPRIIVVDAPDTAAPLAAAAGLGEQVW-LREGRAYAR 5632
QY 525 -----VGPLFWLMAARTVRAREOGTVLLWSGADLRPVSGDPDRAAPLLA---LLHAA 574
Db 5633 RUTPAVPSGDAPEL-----DPDGTVL-----ITGSGTLAGIIVARHLVGHYG 5674
QY 575 PRPLLLLYAFSLCAKGDIP 594
Db 5675 VRRLML---SRGGTASDVP 5691

RESULT 15

Q9HW81 PRELIMINARY; PRT; 523 AA.
AC Q9HW81;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein PA4320.
GN PA4320.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoquchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Coulter S.N., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen";
RL Nature 406:959-964(2000).
RW EMBL; AE004848; AAG07708.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 523 AA; 59671 MW; 56B9F3B1FDB31C91 CRC64;

Query Match 3.0%; Score 105; DB 16; Length 523;
Best Local Similarity 22.2%; Pred. No. 4.4; Mismatches 182; Gaps 25;
Matches 105; Conservative 44; Indels 143;

QY 301 TLRCLPK-----LEAALCQRHDMHTLCKDLP-----NATARES 334
Db 88 TLRQALRAYPALLRQKLPASLLWRRFSPTRSFDPVLQLEGLAGEPQRSRLIVLSQRNAG 147
QY 335 GWYVLEKVDLHPQLCFKVPWFSEFGNSSHVECPHQTGSLTSWNVMDTQAQQLIL---HFS 392
Db 148 GATWLTVVGVHLEMA-----WAGFAMLLYLLIPAQNEIDWNQWSLLDPEAGEWLEHLS 203
QY 393 SRMHATFSAANSLPCLGODTLVPPVY-----TVSQVWRSVQFAWKHLLCPDV 440
Db 204 NLLYVLVLVWME-----PIYVACGFTLYLNRRTLEAW---DIELVFRRL----- 245
QY 441 SYRHIG---LILALALLTLGLVVLALTCRRPQSGPGP---ARPVLLHHAADSEAQRRL 494
Db 246 RQRLVGSAYVLLGLTASLAWL-----PAPSAYAEPA-----AATSAGEAEL 287
QY 495 VGALAEALLRAALG---GGRDV---IVD----- 515
Db 288 PPEQARLLRQKLNSEQAGKQIRAIVDGAPFKNSETVTGWRFQDKTEKKDSRKEDEERLKA 347
QY 516 LWEG-----RHVARV-GPLPW-----LWAAR-----TRVAREOQT 544
Db 348 FFEALANWPFERHAAQVIEVLLWALLFSAVFLLVWRYREWLRFVGNLGLPQARRREAPT 407
QY 545 VLLLSWGADLRPVSGDPDRAAPLLALLHAAAPRPLLLAY---FSRLC-----AK 590
Db 408 VMF---GLDLSPESLPDDIASNAERLNWEXPREALGLLYRGLLSRLLHDYRLPLKGSHT 464
QY 591 GDIPPLRALPRYRLRLDRLPRLLRALDARFAEATSWG-RIGARQRQRSLRLC 643
Db 465 GEVLRLVEGLEQQRPLLYSOLLTAQ-----WQALAYGHRLPADDTTQ---RLC 510

Search completed: January 28, 2003, 09:30:33
Job time : 50 secs